


```

PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 18 AA;

Query Match 62.2%; Score 61; DB 13; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.74e+01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 6 frvdrlrlalry 17
   ||: ||: |||||
QY 1 YRLAIRRIALRY 12

RESULT 3
ID R92911 standard; peptide; 20 AA.
AC R92911;
DT 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526975-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B7-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 53.1%; Score 52; DB 16; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 1 yrlair-lnery 11
   |||||: |||
QY 1 YRLAIRRIALRY 12

RESULT 4
ID R95422 standard; peptide; 25 AA.
AC R95422;
DT 12-NOV-1996 (first entry)
DE HLAB38.6084.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.

PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 18 AA;

Query Match 62.2%; Score 61; DB 13; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.74e+01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 6 frvdrlrlalry 17
   ||: ||: |||||
QY 1 YRLAIRRIALRY 12

RESULT 3
ID R92911 standard; peptide; 20 AA.
AC R92911;
DT 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526975-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B7-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 53.1%; Score 52; DB 16; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 1 yrlair-lnery 11
   |||||: |||
QY 1 YRLAIRRIALRY 12

RESULT 4
ID R95422 standard; peptide; 25 AA.
AC R95422;
DT 12-NOV-1996 (first entry)
DE HLAB38.6084.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.

PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI; 95-194027/25.
PT Compens. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLAB38.6084. These sequences can be used to isolate the protein p74 from
CC a T-cell lysate. p74 is a T-cell surface membrane protein associated
CC with T-cell activation in mammalian T-cells, and is also immunologically
CC cross reactive with the heat shock protein Hsc70. p74 is found in a
CC limited number of cell types, but is particularly expressed on B and T
CC cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 18; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 15 yrenlr-lalry 25
   ||: ||: |||||
QY 1 YRLAIRRIALRY 12

RESULT 5
ID R48286 standard; peptide; 25 AA.
AC R48286;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of HLA-B*38 antigen.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Example 13; Page 39; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide is derived from the HLA-B*38 antigen and corresponds
CC to the amino acid positions 60-84 of that antigen.
SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 8; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 15 yrenlr-lalry 25
   ||: ||: |||||

```

QY 1 YRLAIRRIALRY 12
 RESULT 6
 ID R83093 standard; peptide; 25 AA.
 AC R83093;
 DT 16-MAY-1996 (first entry)
 DE HLAB38 CTL modulating peptide (B38.6084).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLAB38.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 13; Page 32; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLAB38. These sequences can be used to extend the period of acceptance
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides
 CC are administered to a patient in conjunction with a subtherapeutic amount
 CC of an immunosuppressant. This is administered to the patient for a
 CC limited period of time (compared to the lifetime administration for
 CC current treatments). The peptides particularly modulate (or inhibit) the
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
 CC Sequence 25 AA;
 SQ
 Query Match 53.1%; Score 52; DB 16; Length 25;
 Best Local Similarity 66.7%; Pred. No. 1.27e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
 Db 15 yrenlr-ialry 25
 QY 1 YRLAIRRIALRY 12
 RESULT 7
 ID R95415 standard; peptide; 20 AA.
 AC R95415;
 DT 12-NOV-1996 (first entry)
 DE HLA-B7.84-75-84 Palindrome.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 18; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B7.84-75/75-84 palindrome. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity

CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702 60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;
 Query Match 51.0%; Score 50; DB 18; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.94e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Db 6 rlserreslr 15
 QY 2 RLAIIRRIALR 11
 RESULT 8
 ID R92913 standard; peptide; 20 AA.
 AC R92913;
 DT 16-MAY-1996 (first entry)
 DE HLA-B7 CTL modulating peptide (B7.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B7.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B7. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;
 Query Match 51.0%; Score 50; DB 16; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.94e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Db 6 rlserreslr 15
 QY 2 RLAIIRRIALR 11
 RESULT 9
 ID R95425 standard; peptide; 10 AA.
 AC R95425;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702.75-84(D).
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.

```

OS Synthetic.
FH Key Location/Qualifiers
FT MISC-difference 3
FT /note="NSD mutation"
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; UI2985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compens. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 11: 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702.75-84(D). These sequences can be used to isolate the protein
CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 10 AA;

Query Match 50.0%; Score 49; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.40e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 r1alry 10
QY 7 R1ALRY 12

RESULT 10
ID R95413 standard; peptide; 10 AA.
AC R95413;
DE 12-NOV-1996 (first entry)
DE Alpha1-helix of HLA-B2702.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytotoxicity; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; UI2985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compens. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 11: 29pp; English.
CC This sequence represents the alpha1-helix of the
CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,
CC epitopes, and palindromes of it (such as R95428) can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable

```

```

CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 10 AA;

Query Match 50.0%; Score 49; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.40e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 r1alry 10
QY 7 R1ALRY 12

RESULT 11
ID R41208 standard; peptide; 10 AA.
AC R41208;
DE 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI: 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 11; Page 54; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used
CC for inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide sequence is more commonly found within larger peptide
CC compounds of not more than 30 amino acids in length.
SQ Sequence 10 AA;

Query Match 50.0%; Score 49; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.40e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 r1alry 10
QY 7 R1ALRY 12

RESULT 12
ID R95430 standard; peptide; 20 AA.
AC R95430;
DE 12-NOV-1996 (first entry)
DE HLA-B2702 84-75T/75-84T palindromic.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytotoxicity; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; UI2985.

```

PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 human-leucocyte-associated antigens. This sequence represents the
 HLA-B*2702 84-75/75-84 palindromic. These sequences can be used to
 isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 membrane protein associated with T-cell activation in mammalian T-cells,
 and is also immunologically cross reactive with the heat shock protein
 Hsc70. p74 is found in a limited number of cell types, but is
 particularly expressed on B and T cells. p74 can be isolated by lysis of
 a suitable cell with an amphoteric detergent, and then passed through an
 affinity column containing a covalently bound HLA-B*2702 palindromic
 peptide. Compositions comprising the extracellular fragment of p74
 combined with HLA-B*2702.60-84 (see R95416), induces calcium influx, and
 inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.
 CC Candidate compounds can be screened for their effect on the cytolytic
 activity of T-cells, by combining them with the extracellular portion of
 p74 and determining the amount of binding between the candidate compound
 and p74. Modulation of CTL activity can be inhibited in a cellular
 composition containing T-cells and antigen presenting cells (APCs), by
 adding to the mix the extracellular portion of p74, in an amount
 sufficient to compete with p74 for the binding of the p74 ligand.
 CC Sequence 20 AA;

Query Match 50.0%; Score 49; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.40e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
 |||||
 QY 1 YRLAIR 6

RESULT 13
 ID R95428 standard; peptide; 20 AA.
 AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*2702 84-75-84 palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytotoxicity; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 human-leucocyte-associated antigens. These sequences can be used to isolate
 HLA-B*2702 84-75-84 palindromic. These sequences can be used to isolate
 the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 protein associated with T-cell activation in mammalian T-cells, and is
 also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 expressed on B and T cells. p74 can be isolated by lysis of a suitable
 cell with an amphoteric detergent, and then passed through an affinity
 column containing a covalently bound HLA-B*2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
 cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 T-cells, by combining them with the extracellular portion of p74 and

CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 50.0%; Score 49; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.40e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
 |||||
 QY 1 YRLAIR 6

RESULT 14
 ID R05012 standard; protein; 20 AA.
 AC R05012;
 DT 03-OCT-1990 (first entry)
 DE Papilloma virus type 16 L2 peptide no. 55.
 KW Papilloma virus; PV type 16; immunoglobulin; L2; ELISA: cervical cancer.
 OS Synthetic.
 PN WO9004790-A.
 PD 03-MAY-1990.
 PR 30-OCT-1989; SE0612.
 PR 28-OCT-1989; SE-003870.
 PA (MEDS-) Medscand AB.
 PI Dillner J, Dillner L;
 DR WPI: 90-164122/21.
 PT Detecting papilloma virus infections - by identifying specific
 PT antibodies against partic. viral proteins or fragments, esp. for
 PT rapid diagnosis of cervical cancer.
 PS Disclosure; 7pp; English.
 CC The peptide is one of 66 overlapping peptides which together cover
 CC the entire sequences of the L1 and L2 proteins of human PV type 16.
 CC The peptide was found to be unreactive with Ig Abs in the sera of
 CC patients with type 16 cervical cancer.
 CC See also R04958-R05023.
 SQ Sequence 20 AA;

Query Match 50.0%; Score 49; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.40e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 8 ltsrrtgirly 17
 | : || : ||
 QY 3 LAIRRIALRY 12

RESULT 15
 ID R95416 standard; peptide; 25 AA.
 AC R95416;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*2702.60-84.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytotoxicity; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 human-leucocyte-associated antigens. This sequence represents
 CC HLA-B*2702.60-84. These sequences can be used to isolate the protein p74.

CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC this sequence, induces calcium influx, and inhibits cytotoxic T
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can
 CC be screened for their effect on the cytotoxic activity of T-cells, by
 CC combining them with the extracellular portion of p74 and determining the
 CC amount of binding between the candidate compound and p74. Modulation of
 CC CTL activity can be inhibited in a cellular composition containing
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the
 CC extracellular portion of p74, in an amount sufficient to compete with p74
 CC for the binding of the p74 ligand.
 SQ Sequence 25 AA;

Query Match 50.0%; Score 49; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.40e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 r1alry 25
 QY 7 R1ALRY 12

Search completed: Thu May 22 08:50:42 1997
 Job time : 6 secs.

MPSEARCH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:36:18 1997; MasPar time 2.92 Seconds
Tabular output not generated. 116.962 Million cell updates/sec

Title: >US-08-653-294-36
Description: (1-12) from US08653294.pep
Perfect Score: 98
Sequence: 1 YRLAIRRLRY 12

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 26.905; Variance 45.950; scale 0.586

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description | Pred. No. |
|------------|-------|---------------|--------|----|------------------------|-----------|
| 1 | 63 | 64.3 | 128 | 11 | hypothetical protein | 2.74e+00 |
| 2 | 58 | 59.2 | 388 | 16 | hypothetical protein | 1.59e+01 |
| 3 | 57 | 58.2 | 281 | 10 | strf protein - Strep | 2.23e+01 |
| 4 | 57 | 58.2 | 348 | 6 | histocompatibility a | 2.23e+01 |
| 5 | 56 | 57.1 | 78 | 10 | DNA-directed RNA pol | 3.13e+01 |
| 6 | 56 | 57.1 | 416 | 3 | nicotinic acetylcholin | 3.13e+01 |
| 7 | 56 | 57.1 | 495 | 16 | acetylcholine recept | 3.13e+01 |
| 8 | 56 | 57.1 | 499 | 7 | nicotinic acetylcholin | 3.13e+01 |
| 9 | 56 | 57.1 | 503 | 7 | nicotinic acetylcholin | 3.13e+01 |
| 10 | 56 | 57.1 | 788 | 12 | COI intron alpha-sen | 3.13e+01 |
| 11 | 56 | 57.1 | 1151 | 11 | GRR1 protein - yeast | 3.13e+01 |
| 12 | 55 | 56.1 | 176 | 14 | gene RXRbeta1 protei | 4.36e+01 |
| 13 | 55 | 56.1 | 212 | 11 | hypothetical protein | 4.36e+01 |
| 14 | 55 | 56.1 | 281 | 10 | strf protein - Strep | 4.36e+01 |
| 15 | 55 | 56.1 | 491 | 3 | nicotinic acetylcholin | 4.36e+01 |
| 16 | 55 | 56.1 | 493 | 7 | nicotinic acetylcholin | 4.36e+01 |
| 17 | 55 | 56.1 | 511 | 10 | hypothetical protein | 4.36e+01 |
| 18 | 55 | 56.1 | 583 | 8 | chaperonin-60 alpha | 4.36e+01 |
| 19 | 55 | 56.1 | 1420 | 5 | apolipoprotein(a) (E | 4.36e+01 |
| 20 | 55 | 56.1 | 2242 | 12 | pyrimidine synthesis | 4.36e+01 |
| 21 | 54 | 55.1 | 267 | 16 | strf protein - Strep | 6.05e+01 |

22 54 55.1 267 10 S44228 strf protein - Strep 6.05e+01
23 54 55.1 298 12 S53849 ribosomal protein S3 6.05e+01
24 54 55.1 462 11 S53114 hypothetical protein 6.05e+01
25 54 55.1 493 3 ACNSE nicotinic acetylcholin 6.05e+01
26 54 55.1 493 3 ACNSE nicotinic acetylcholin 6.05e+01
27 54 55.1 500 7 S12899 nicotinic acetylcholin 6.05e+01
28 54 55.1 651 9 S47750 hypothetical protein 6.05e+01
29 54 55.1 699 1 WQBSGS phosphotransferase s 6.05e+01
30 54 55.1 850 12 S20462 RNA12 protein - yeast 6.05e+01
31 54 55.1 880 5 B33926 DNA-directed RNA pol 6.05e+01
32 54 55.1 880 5 S04717 DNA-directed RNA pol 6.05e+01
33 54 55.1 1748 1 JQ1555 RNA-directed RNA pol 6.05e+01
34 53 54.1 203 11 S50980 NHP10 protein - yeast 8.37e+01
35 53 54.1 252 16 I48120 p-glycoprotein - ham 8.37e+01
36 53 54.1 259 16 I48119 p-glycoprotein - ham 8.37e+01
37 53 54.1 324 13 S43424 zipper containing pr 8.37e+01
38 53 54.1 334 10 I40338 biotin synthetase - 8.37e+01
39 53 54.1 454 7 B39218 nicotinic acetylcholin 8.37e+01
40 53 54.1 508 1 TVUT4B phosphoglycerate kin 8.37e+01
41 53 54.1 622 3 ACCH4N nicotinic acetylcholin 8.37e+01
42 53 54.1 1281 14 I48123 p-glycoprotein isofo 8.37e+01
43 53 54.1 1858 4 A44214 genome polyprotein 1 8.37e+01
44 53 54.1 3391 4 GNMV16 genome polyprotein - 8.37e+01
45 53 54.1 3391 4 GNMV26 genome polyprotein - 8.37e+01

ALIGNMENTS

RESULT 1
ENTRY #type complete
TITLE hypothetical protein YDR360w - yeast (Saccharomyces cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 06-Sep-1996
ACCESSIONS S69745
REFERENCE S69745
#authors Du, Z.
#submission submitted to the EMBL Data Library, June 1995
#description The sequence of S. cerevisiae cosmid 9476.
#accession S69745
#molecule_type DNA
#residues 1-128 #label DUZ
#cross-references EMBL:U28372
GENETICS
#map_position 4R
SUMMARY #length 128 #molecular-weight 14014 #checksum 3949
Query Match 64.3%; Score 63; DB 11; Length 128;
Best Local Similarity 54.5%; Pred. No. 2.74e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 113 yilsvrrltlr 123
QY 1 YRLAIRRLRY 11
RESULT 2
ENTRY #type complete
TITLE hypothetical protein (insertion sequence ISH27-3) - Halobacterium halobium
ORGANISM #formal_name Halobacterium halobium
DATE 21-Nov-1993 #sequence_revision 21-Nov-1993 #text_change 21-Nov-1993
ACCESSIONS S15593
REFERENCE S15593
#authors Pfeiffer, F.; Blaselo, U.
#journal Nucleic Acids Res. (1990) 18:6921-6925
#title Transposition burst of the ISH27 insertion element family in Halobacterium halobium.
#cross-references MUID:91088266
#accession S15593
#status preliminary

```

##residues 1-388 ##label PFE
##cross-references EMBL:X54434
SUMMARY #length 388 #molecular-weight 44571 #checksum 1952

Query Match 59.2%; Score 58; DB 16; Length 388;
Best Local Similarity 75.0%; Pred. No. 1.59e+01;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 154 yrlavrrl 161
   |||||:|:|
QY 1 YRLAIRRI 8

RESULT 3
ENTRY #type complete
TITLE strF protein - Streptomyces griseus
ORGANISM #formal_name Streptomyces griseus
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
23-Mar-1993
ACCESSIONS S17776
REFERENCE Mansouri, K.; Piepersberg, W.
#authors Mol. Gen. Genet. (1991) 228:459-469
#journal Genetics of streptomycin production in Streptomyces griseus:
#title nucleotide sequence of five genes, strFGHIK, including a
phosphatase gene.
#cross-references MUID:91375432
#accession S17776
##status not compared with conceptual translation
##residues 1-281 ##label MAN
GENETICS
#gene strF
#start_codon GTG
SUMMARY #length 281 #molecular-weight 31726 #checksum 5011

Query Match 58.2%; Score 57; DB 10; Length 281;
Best Local Similarity 70.0%; Pred. No. 2.23e+01;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 234 rlaarllamr 243
   |||||:|:|
QY 2 RLAIRRIALR 11

RESULT 4
ENTRY #type complete
TITLE histocompatibility antigen, HLA-F-like - rhesus macaque
ORGANISM #formal_name Macaca mulatta #common_name rhesus macaque
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
26-Apr-1996
ACCESSIONS S29990
REFERENCE Bontrorp, R.R.
#authors Submissions submitted to the EMBL Data Library, February 1993
#accession S29990
##status preliminary
##molecule_type mRNA
##residues 1-348 ##label BON
##cross-references EMBL:Z21819
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
219-284 #domain immunoglobulin homology #label IMM
SUMMARY #length 348 #molecular-weight 39300 #checksum 5372

Query Match 58.2%; Score 57; DB 6; Length 348;
Best Local Similarity 54.5%; Pred. No. 2.23e+01;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 98 rvalrklilly 108
   |||||:|:|
QY 2 RLAIRRIALRY 12

```

```

RESULT 5
ENTRY #type complete
TITLE DNA-directed RNA polymerase (EC 2.7.7.6) subunit H -
Methanococcus jannaschii
ORGANISM #formal_name Methanococcus jannaschii
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
13-Sep-1996
ACCESSIONS F64429
REFERENCE A64300
#authors Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann,
R.D.; Sutton, G.G.; Blake, J.A.; Fitzgerald, L.M.; Clayton,
R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.;
Tombl, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann,
J.L.; Nguyen, D.; Uterback, T.R.; Kelley, J.M.; Peterson,
J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts,
K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk,
H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
#journal Science (1996) 273:1058-1073
#title Complete genome sequence of the methanogenic archaeon,
Methanococcus jannaschii.
#accession F64429
##status preliminary; nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-78 ##label BUL
##cross-references GB:L77117; TIGR:MTJ1039; CDS_PID:g1511063
GENETICS
#map_position FOR970764-971000
#start_codon TTG
#nucleotidyltransferase
SUMMARY #length 78 #molecular-weight 9001 #checksum 3754

Query Match 57.1%; Score 56; DB 10; Length 78;
Best Local Similarity 75.0%; Pred. No. 3.13e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 70 yrlvlkrl 77
   |||||:|:|
QY 1 YRLAIRRI 8

RESULT 6
ENTRY #type fragment
TITLE nicotinic acetylcholine receptor alpha-3 chain, neuronal -
chicken (fragment)
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
09-Sep-1994
ACCESSIONS S00378; A38755
REFERENCE S00378
#authors Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
#journal EMBO J. (1988) 7:595-601
#title Genes expressed in the brain define three distinct neuronal
nicotinic acetylcholine receptors.
#cross-references MUID:88283624
#accession S00378
##molecule_type DNA; mRNA
##residues 1-416 ##label NEF
##cross-references EMBL:X07345
GENETICS
#introns 37/2; 374/3
CLASSIFICATION #superfamily acetylcholine receptor
KEYWORDS glycoprotein; ion channel; neurotransmitter receptor;
postsynaptic membrane; transmembrane protein
FEATURE
153-176 #domain transmembrane #status predicted #label TM1\
184-202 #domain transmembrane #status predicted #label TM2\
218-239 #domain transmembrane #status predicted #label TM3\
389-407 #domain transmembrane #status predicted #label TM4\

```

```

70-84,134-135 #disulfide_bonds #status predicted\
83,295,329 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 416 #checksum 3404

Query Match 57.1%; Score 56; DB 3; Length 416;
Best Local Similarity 58.3%; Pred. No. 3.13e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 144 yslvirrlply 155
| | | | | | | |
| | | | | | | |
1 YRLAIRRLRY 12

RESULT 7
ENTRY #type complete
TITLE acetylcholine receptor alpha chain precursor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 27-Apr-1996 #sequence_revision 27-Apr-1996 #text_change
27-Apr-1996
ACCESSIONS S60589
REFERENCE S60589
#authors Criado, M.; Alamo, L.; Navarro, A.
#journal Neurochem. Res. (1992) 17:281-287
#title Primary structure of an agonist binding subunit of the
nicotinic acetylcholine receptor from bovine adrenal
chromaffin cells.
#accession S60589
#status preliminary
#residues 1-495 #label CRI
#cross-references EMBL:X57032
SUMMARY #length 495 #molecular-weight 56914 #checksum 5081

Query Match 57.1%; Score 56; DB 15; Length 495;
Best Local Similarity 58.3%; Pred. No. 3.13e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 223 yslvirrlply 234
| | | | | | | |
| | | | | | | |
1 YRLAIRRLRY 12

RESULT 8
ENTRY #type complete
TITLE nicotinic acetylcholine receptor alpha-3 chain precursor -
rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
15-Jun-1996
ACCESSIONS A24572
REFERENCE A24572
#authors Boulter, J.; Evans, K.; Goldman, D.; Martin, G.; Treco, D.;
Heinemann, S.; Patrick, J.
#journal Nature (1986) 319:368-374
#title Isolation of a cDNA clone coding for a possible neural
nicotinic acetylcholine receptor alpha-subunit.
#cross-references MUID:86118671
#accession A24572
#molecule_type mRNA
#residues 1-499 #label BOU
CLASSIFICATION #superfamily acetylcholine receptor
KEYWORDS glycoprotein; ion channel; neurotransmitter receptor;
postsynaptic membrane; transmembrane protein
FEATURE
1-25 #domain signal sequence #label SIG\
26-499 #product nicotinic acetylcholine receptor alpha chain
#label NAT
SUMMARY #length 499 #molecular-weight 57347 #checksum 1936

Query Match 57.1%; Score 56; DB 7; Length 499;
Best Local Similarity 58.3%; Pred. No. 3.13e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Db 227 yslvirrlply 238
| | | | | | | |
| | | | | | | |
1 YRLAIRRLRY 12

RESULT 9
ENTRY #type complete
TITLE nicotinic acetylcholine receptor alpha-3 chain precursor,
neuronal - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
08-Sep-1996
ACCESSIONS A53956; S21338
REFERENCE A53956
#authors Mihovilovic, M.; Roses, A.D.
#journal Exp. Neurol. (1991) 111:175-180
#title Expression of mRNAs in human thymus coding for the alpha3
subunit of a neuronal acetylcholine receptor.
#accession A53956
#status preliminary
#molecule_type mRNA
#residues 1-503 #label MIH
#cross-references GB:M37981
REFERENCE S21338
#authors Anand, R.; Lindstrom, J.
#submission submitted to the EMBL Data Library, June 1990
#description Nucleotide sequence of the mature human nicotinic
acetylcholine receptor beta-3 subunit gene.
#accession S21338
#status preliminary
#molecule_type mRNA
#residues 30-503 #label ANA
#cross-references EMBL:X53559
GENETICS GDB:CHRNA3
#gene
#cross-references GDB:125219
#map_position 15q24-15q24
CLASSIFICATION #superfamily acetylcholine receptor
SUMMARY #length 503 #molecular-weight 57153 #checksum 8851

Query Match 57.1%; Score 56; DB 7; Length 503;
Best Local Similarity 58.3%; Pred. No. 3.13e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 231 yslvirrlply 242
| | | | | | | |
| | | | | | | |
1 YRLAIRRLRY 12

RESULT 10
ENTRY #type complete
TITLE COI intron alpha-sen DNA protein - Podospora anserina
mitochondrion (SGC3)
ORGANISM #formal_name mitochondrion Podospora anserina
DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
17-Feb-1994
ACCESSIONS B48327
REFERENCE A48327
#authors Cummings, D.J.; Michel, F.; McNally, K.L.
#journal Curr. Genet. (1989) 16:381-406
#title DNA sequence analysis of the 24.5 kilobase pair cytochrome
oxidase subunit I mitochondrial gene from Podospora
anserina: a gene with sixteen introns.
#accession B48327
#status preliminary
#molecule_type DNA
#residues 1-788 #label CUM
#cross-references GB:X55026; GB:M30937; GB:M61734
GENETICS
#genome mitochondrion
#genetic_code SGC3
KEYWORDS mitochondrion
SUMMARY #length 788 #molecular-weight 89463 #checksum 3000

```

```
Query Match          57.1%; Score 56; DB 12; Length 788;
Best Local Similarity 70.0%; Pred. No. 3.13e+01;
Matches              7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 598 lpirdilrly 607
      ||| |||
QY 3 LAIRRIALRY 12

RESULT 11
ENTRY GRRI protein - yeast (Saccharomyces cerevisiae)
TITLE protein J1885; protein YJR090c
ALTERNATE_NAMES #formal name Saccharomyces cerevisiae
ORGANISM 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
DATE 13-Sep-1995
ACCESSIONS A41529; S57109; S57111; S17487
REFERENCE A41529
#authors Flick, J.S.; Johnston, M.
#journal Mol. Cell. Biol. (1991) 11:5101-5112
#title GRRI of Saccharomyces cerevisiae is required for glucose
#cross-references MUID:92017785 repression and encodes a protein with leucine-rich repeats.
#accession A41529
#molecule_type DNA
#residues 1-1151 #label FLI
#cross-references GB:M59247
REFERENCE S57085
#authors Manus, V.; Huang, M.E.; Galibert, F.
#submission submitted to the Protein Sequence Database, September 1995
#accession S57109
#molecule_type DNA
#residues 1-1151 #label MAN
#cross-references EMBL:249590
REFERENCE S57111
#authors Ramezani Rad, M.; Kirchrath, L.; Hollenberg, C.P.
#submission submitted to the Protein Sequence Database, September 1995
#accession S57111
#molecule_type DNA
#residues 1-2 #label RAM
#cross-references EMBL:249590
GENETICS
#gene LISTA:GRR1
#map_position 10R
KEYWORDS tandem repeat
FEATURE
409-725
SUMMARY #length 1151 #molecular-weight 132733 #checksum 1173

Query Match          57.1%; Score 56; DB 11; Length 1151;
Best Local Similarity 41.7%; Pred. No. 3.13e+01;
Matches              5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 386 yrimikrlnfsf 397
      ||| ||| :
QY 1 YRLAIRRIALRY 12

RESULT 12
ENTRY gene RXRBeta1 protein - mouse (fragment)
TITLE #formal name Mus musculus #common name house mouse
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 02-Jul-1996
ACCESSIONS I48752
REFERENCE I48752
#authors Nagata, T.; Kanno, Y.; Ozato, K.; Taketo, M.
#journal Gene (1994) 142:183-189
#title The mouse Rxrb gene encoding RXR beta: genomic organization
#cross-references MUID:94252565 and two mRNA isoforms generated by alternative splicing of
transcripts initiated from CpG island promoters.
```

```
#accession I48752
#status preliminary; translated from GB/EMBL/DBAJ
#molecule_type DNA
#residues 1-176 #label RES
#cross-references EMBL:X72017; NID:g510152; CDS-PID:g510153
GENETICS
#introns 76/1; 137/2
#note gene name RXRBeta1
SUMMARY #length 176 #checksum 8478

Query Match          56.1%; Score 55; DB 14; Length 176;
Best Local Similarity 66.7%; Pred. No. 4.36e+01;
Matches              6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 125 lqirrlslr 133
      ||| ||| :
QY 3 LAIRRIALR 11

RESULT 13
ENTRY S17476 #type complete
TITLE hypothetical protein YCL034w - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein YCL186
ORGANISM #formal name Saccharomyces cerevisiae
DATE 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
ACCESSIONS S17476; S19362
REFERENCE S17471
#authors Ramezani Rad, M.; Luetzenkirchen, K.; Xu, G.; Kleinhans, U.;
#journal Hollenberg, C.P.
#title Yeast (1991) 7:533-538
#accession S17476
#status translation not shown
#molecule_type DNA
#residues 1-212 #label RAM
#cross-references EMBL:X59720
REFERENCE S19350
#authors Hollenberg, C.P.; Kleinhans, U.; Lutzenkirchen, K.; Ramezani
#submission submitted to the Protein Sequence Database, March 1992
#accession S19362
#molecule_type DNA
#residues 1-212 #label HOL
#cross-references EMBL:X59720
GENETICS
#map_position 3L
SUMMARY #length 212 #molecular-weight 23590 #checksum 526

Query Match          56.1%; Score 55; DB 11; Length 212;
Best Local Similarity 77.8%; Pred. No. 4.36e+01;
Matches              7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 115 airrkvlry 123
      ||| |||
QY 4 AIRRIALRY 12

RESULT 14
ENTRY S44230 #type complete
TITLE strf protein - Streptomyces glaucescens
ORGANISM #formal name Streptomyces glaucescens
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
ACCESSIONS S44230
REFERENCE S44230
#authors Mayer, G.; Piepersberg, W.
#submission submitted to the EMBL Data Library, April 1994
#accession S44230
#status preliminary
#molecule_type DNA
```

```
##residues 1-281 ##label MAY
##cross-references EMBL:X78974
GENETICS
#start_codon GTG
SUMMARY #length 281 #molecular-weight 31427 #checksum 4100
Query Match 56.1%; Score 55; DB 10; Length 281;
Best Local Similarity 70.0%; Pred. No. 4.36e+01;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 234 riaarlr 243
| | | | |
QY 2 RLAIIRIALR 11

RESULT 15
ENTRY ACBOE #type complete
TITLE nicotinic acetylcholine receptor epsilon chain precursor -
ORGANISM bovine
#formal_name Bos primigenius taurus #common_name cattle
DATE 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change
08-Dec-1994
ACCESSIONS A03174
REFERENCE A03174
#authors Takai, T.; Noda, M.; Mishina, M.; Shimizu, S.; Furutani, Y.;
Kayano, T.; Ikeda, T.; Kubo, T.; Takahashi, H.; Takahashi,
T.; Kuno, M.; Numa, S.
#journal Nature (1985) 315:761-764
#title Cloning, sequencing and expression of cDNA for a novel
subunit of acetylcholine receptor from calf muscle.
#cross-references MUID:85240565
#accession A03174
##molecule_type mRNA
##residues 1-491 ##label TAK
COMMENT The epsilon chain can replace the gamma chain to form a functional
receptor molecule.
CLASSIFICATION #superfamily acetylcholine receptor
KEYWORDS glycoprotein; ion channel; neurotransmitter receptor;
postsynaptic membrane; transmembrane protein
FEATURE
1-20 #domain signal sequence #status predicted #label SIG\
21-491 #product acetylcholine receptor epsilon chain #status
predicted #label MAT\
240-266 #domain transmembrane #status predicted #label TM1\
273-291 #domain transmembrane #status predicted #label TM2\
307-328 #domain transmembrane #status predicted #label TM3\
420-436 #domain transmembrane amphipathic helix #status
predicted #label TMH\
457-480 #domain transmembrane #status predicted #label TM4\
86,161,327 #binding_site carbohydrate (Asn) (covalent) #status
predicted\
148-162 #disulfide_bonds #status predicted
SUMMARY #length 491 #molecular-weight 54565 #checksum 7419
Query Match 56.1%; Score 55; DB 3; Length 491;
Best Local Similarity 58.3%; Pred. No. 4.36e+01;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Db 232 yslirrkplfy 243
| | | | |
QY 1 YRLAIRIALRY 12
```

Search completed: Thu May 22 08:36:46 1997
Job time : 28 secs.

THIS PAGE BLANK (USPTO)

WIREH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligent, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:34:07 1997; MasPar time 2.32 Seconds
Tabular output not generated. 182.533 Million cell updates/sec

Title: >US-08-653-294-31
Description: (1-20) from US08653294.pep
Perfect Score: 154
Sequence: 1 YRLAIRLNEYRLAIRLNER 20

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 30.299; Variance 54.375; scale 0.557

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|----------------------------------|-----------|
| 1 | 71 | 46.1 | 361 | 3 | FDH_PSEPU 5-EXO-ALCOHOL DEHYDRO | 9.83e+01 |
| 2 | 70 | 45.5 | 279 | 5 | LEP3_ERWCA TYPE 4 PREPILIN-LIKE | 1.38e+00 |
| 3 | 70 | 45.5 | 782 | 3 | DPO2_ECOLI DNA POLYMERASE II (EC | 1.38e+00 |
| 4 | 68 | 44.2 | 252 | 8 | PYG4_ANASP PHYCOBILISOME ROD-COR | 2.71e+00 |
| 5 | 68 | 44.2 | 253 | 8 | PYG3_MASLA PHYCOBILISOME ROD-COR | 2.71e+00 |
| 6 | 68 | 44.2 | 349 | 6 | NTRB_ECOLI NITROGEN REGULATION P | 2.71e+00 |
| 7 | 68 | 44.2 | 1051 | 5 | ITR3_CRISP INTEGRIN ALPHA-3 PREC | 2.71e+00 |
| 8 | 68 | 44.2 | 1051 | 5 | ITR3_HUMAN INTEGRIN ALPHA-3 PREC | 2.71e+00 |
| 9 | 67 | 43.5 | 346 | 8 | RFAP_HAEIN ADP-HEPTOSE--LPS HEPT | 3.77e+00 |
| 10 | 67 | 43.5 | 424 | 11 | YQ05_CAEEL HYPOTHETICAL 48.0 KD | 3.77e+00 |
| 11 | 65 | 42.2 | 349 | 6 | NTRB_SALTY NITROGEN REGULATION P | 7.24e+00 |
| 12 | 65 | 42.2 | 643 | 2 | CR72_BACTI 72 KD CRYSTAL PROTEIN | 7.24e+00 |
| 13 | 64 | 41.6 | 648 | 1 | BGR_RAT BETA-GLUCURONIDASE PR | 9.99e+00 |
| 14 | 64 | 41.6 | 1104 | 6 | NIR_EMENT NITRATE REDUCTASE (NA | 9.99e+00 |
| 15 | 64 | 41.6 | 3224 | 6 | N358_HUMAN NUCLEAR PORE COMPLEX | 9.99e+00 |
| 16 | 63 | 40.9 | 115 | 10 | VG52_HSVSA HYPOTHETICAL GENE 52 | 1.37e+01 |
| 17 | 63 | 40.9 | 485 | 10 | VGLC_HSV4 GLYCOPROTEIN C PRECUR | 1.37e+01 |
| 18 | 63 | 40.9 | 580 | 4 | GPC3_HUMAN GLYPICAN-3 PRECURSOR | 1.37e+01 |
| 19 | 63 | 40.9 | 597 | 4 | GPC3_RAT GLYPICAN-3 PRECURSOR | 1.37e+01 |
| 20 | 63 | 40.9 | 648 | 1 | AMT_PYRFU ALPHA-AMYLASE (EC 3.2 | 1.37e+01 |
| 21 | 62 | 40.3 | 253 | 7 | PKNA_MYCLE PROTEIN KINASE PKNA. | 1.88e+01 |
| 22 | 62 | 40.3 | 293 | 8 | RL5_SCHPO 60S RIBOSOMAL PROTEIN | 1.88e+01 |

| | | | | | | |
|----|----|------|------|----|-----------------------------------|----------|
| 23 | 62 | 40.3 | 558 | 10 | VP10_RBSDV PROTEIN S10. | 1.88e+01 |
| 24 | 62 | 40.3 | 818 | 9 | SAP4_YEAST SITA-ASSOCIATING PROT | 1.88e+01 |
| 25 | 62 | 40.3 | 1176 | 6 | NIR_NEUCR NITRATE REDUCTASE (NA | 1.88e+01 |
| 26 | 61 | 39.6 | 239 | 3 | CYSH_THIRO 3'-PHOSPHOADENOSINE 5 | 2.57e+01 |
| 27 | 61 | 39.6 | 354 | 4 | FUT2_RABIT GALACTOSIDE 2-L-FUCOS | 2.57e+01 |
| 28 | 61 | 39.6 | 358 | 11 | YV29_MYCTU HYPOTHETICAL 39.3 KD | 2.57e+01 |
| 29 | 61 | 39.6 | 587 | 7 | PH84_YEAST INORGANIC PHOSPHATE T | 2.57e+01 |
| 30 | 61 | 39.6 | 635 | 9 | TPOR_HUMAN THROMBOPOIETIN RECEPT | 2.57e+01 |
| 31 | 61 | 39.6 | 685 | 9 | TGLC_MOUSE PROTEIN-GLUTAMINE GAM | 2.57e+01 |
| 32 | 61 | 39.6 | 687 | 9 | TGLC_BOVIN PROTEIN-GLUTAMINE GAM | 2.57e+01 |
| 33 | 61 | 39.6 | 881 | 4 | GAL4_YEAST REGULATORY PROTEIN GA | 2.57e+01 |
| 34 | 61 | 39.6 | 907 | 1 | AVRA_PSESG AVIRULENCE A PROTEIN. | 2.57e+01 |
| 35 | 61 | 39.6 | 928 | 8 | RE_HUMAN RETINOBLASTOMA-ASSOCI | 2.57e+01 |
| 36 | 61 | 39.6 | 1483 | 3 | CYPL1_YEAST CYPL1 ACTIVATOR PROTE | 2.57e+01 |
| 37 | 61 | 39.6 | 3712 | 1 | ACVS_CEPAC DELTA-(L-ALPHA-AMINO | 2.57e+01 |
| 38 | 60 | 39.0 | 114 | 10 | UR96_HSVU PROTEIN U58. | 3.49e+01 |
| 39 | 60 | 39.0 | 314 | 9 | TRUB_ECOLI TRNA PSEUDOURIDINE 55 | 3.49e+01 |
| 40 | 60 | 39.0 | 337 | 3 | DFRA_VITVI DIHYDROFLAVONOL-4-RED | 3.49e+01 |
| 41 | 60 | 39.0 | 367 | 11 | YV29_MYCLE HYPOTHETICAL 40.5 KD | 3.49e+01 |
| 42 | 60 | 39.0 | 396 | 7 | P53_SALIR CELLULAR TUMOR ANTIGE | 3.49e+01 |
| 43 | 60 | 39.0 | 622 | 5 | KUP_ECOLI KUP SYSTEM POTASSIUM | 3.49e+01 |
| 44 | 60 | 39.0 | 693 | 8 | RECG_HAEIN ATP-DEPENDENT DNA HEL | 3.49e+01 |
| 45 | 60 | 39.0 | 921 | 8 | RE_HUMAN RETINOBLASTOMA-ASSOCI | 3.49e+01 |

ALIGNMENTS

| RESULT | 1 | STANDARD; | PRT; | 361 | AA. |
|-------------|--|-----------|-------|-------------|-----|
| ID | FDH_PSEPU | | | | |
| AC | P09347; | | | | |
| DT | 01-MAR-1989 (REL. 10, CREATED) | | | | |
| DT | 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) | | | | |
| DT | 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) | | | | |
| DE | 5-EXO-ALCOHOL DEHYDROGENASE (EC 1.1.1.-) (FDEH). | | | | |
| GN | CAND. | | | | |
| OS | PSEUDOMONAS PUTIDA. | | | | |
| OC | PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI; | | | | |
| ON | PSEUDOMONADACEAE. | | | | |
| RC | SEQUENCE FROM N.A., AND REVISIONS TO 97-100. | | | | |
| RC | STRAIN=ATCC 17453; | | | | |
| RX | MEDLINE; 93326643. | | | | |
| RA | ARAKI H., KOGA H., SAGARA Y., HOSOI M., HORIUCHI T.; | | | | |
| RA | BIOCHIM. BIOPHYS. ACTA 1174:91-94(1993). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 1-100 FROM N.A., AND SEQUENCE OF 1-45. | | | | |
| RC | STRAIN=ATCC 17453; | | | | |
| FX | MEDLINE; 86223770. | | | | |
| RA | KOGA H., ARAKI H., YAMAGUCHI E., TAKEUCHI K., HORIUCHI T.; | | | | |
| RA | GUNSALUS I.C.; | | | | |
| RL | J. BACTERIOL. 166:1089-1095(1986). | | | | |
| CC | -1- CATALYTIC ACTIVITY: 5-EXO-HYDROXYCAMPHOR + NAD(+) = | | | | |
| CC | 2,5-DIKETOCAMPHOR + NADH. | | | | |
| CC | -1- COFACTOR: THIS IS A ZINC-CONTAINING DEHYDROGENASE. | | | | |
| CC | -1- PATHWAY: SECOND STEP FOR CATABOLISM OF CAMPHOR. | | | | |
| CC | -1- INDUCTION: BY CAMPHOR. | | | | |
| CC | -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY. | | | | |
| DR | EMBL; D14680; G473746; .. | | | | |
| DR | EMBL; M13471; G551925; ALT_SEQ. | | | | |
| DR | PIR; A29844; A29844. | | | | |
| DR | HSSP; P00327; 1ADF. | | | | |
| DR | PROSITE; PS00059; ADH_ZINC. | | | | |
| KW | OXIDOREDUCTASE; ZINC; NAD. | | | | |
| FT | METAL 40 40 | | | | |
| FT | METAL 62 62 | | | | |
| FT | METAL 98 98 | | | | |
| FT | METAL 101 101 | | | | |
| FT | METAL 104 104 | | | | |
| FT | METAL 170 170 | | | | |
| SQ | SEQUENCE 361 AA; 38460 MW; E46D28F7 CRC32; | | | | |
| Query Match | 46.1%; | Score 71; | DB 3; | Length 361; | |

```

RL  MOL. GEN. GENET. 226:24-33(1991).
[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN-K12;
RX  MEDLINE; 91083835.
RA  CHEN H., SUN Y., STARK T., BEATTIE W., MOSES R.E.;
RL  DNA CELL BIOL. 9:631-635(1990).
[3]
RN  SEQUENCE FROM N.A.
RP  STRAIN-K12;
RX  MEDLINE; 92334977.
RA  YURA T., MORI H., NAGAI H., NAGATA T., ISHIHAMA A., FUJITA N.,
RA  ISONO K., MIZOBUCHI K., NAKATA A.;
RL  NUCLEIC ACIDS RES. 20:3305-3308(1992).
[4]
RN  SEQUENCE OF 1-457 FROM N.A., AND SEQUENCE OF 1-27.
RP  STRAIN-K12;
RX  MEDLINE; 91017565.
RA  BONNER C.A., HAYS S., MCENTEE K., GOODMAN M.F.;
RL  PROC. NATL. ACAD. SCI. U.S.A. 87:7663-7667(1990).
CC  -1- FUNCTION: THOUGHT TO BE INVOLVED IN DNA REPAIR AND/OR MUTAGENESIS.
CC  -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
CC  N PYROPHOSPHATE + DNA(N).
CC  -1- ENZYME REGULATION: DNA POLYMERASE II ACTIVITY IS REGULATED BY
CC  THE LEXA GENE DURING THE SOS RESPONSE.
CC  -1- SIMILARITY: BELONGS TO FAMILY B OF DNA POLYMERASES.
DR  EMBL; X54847; G581193; -
DR  EMBL; M37727; G145746; -
DR  EMBL; M62646; G147318; -
DR  EMBL; M35371; E27155; ALT_SEQ.
DR  EMBL; M38283; G705349; -
DR  EMBL; D10483; G285766; -
DR  PIR; S15943; JDEC22.
DR  PIR; B36236; B36236.
DR  PIR; JQ0780; JQ0780.
DR  PIR; S19263; S19263.
DR  ECOGENE; EG10747; POLB.
DR  PROSITE; PS00116; DNA_POLYMERASE_B.
KW  DNA-DIRECTED DNA POLYMERASE; SOS RESPONSE; DNA REPAIR; DNA-BINDING.
FT  INIT_MET 0 0
FT  CONFLICT 171 171 G -> A (IN REF. 2).
FT  CONFLICT 256 257 EH -> DD (IN REF. 4).
FT  CONFLICT 271 271 R -> G (IN REF. 4).
FT  CONFLICT 734 734 N -> T (IN REF. 2).
FT  CONFLICT 739 782 LQVPSPLDYHYVLTQLQPVAGILPFIEDNFFATL
FT  MTQGLGIF -> PGLPTFTGLTSLDPPATTRGG
FT  NTPFY (IN REF. 2).
SQ  SEQUENCE 782 AA; 89921 MW; 0762928E CRC32;

Query Match 45.5%; Score 70; DB 3; Length 782;
Best Local Similarity 50.0%; Pred. No. 1.38e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 230 rmlqkhaeryrlplrl 245
| : |||||:|
QY 2 RLAILNERYRLAIRL 17

RESULT 4
ID PYG4_ANASP STANDARD; PRT 252 AA.
AC P2989;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG4 (L-RC 29.2).
GN CPCG4.
OS ANABAENA SP. (STRAIN PCC 7120).
OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
OC CYANOBACTERIA (BLUE-GREEN ALGAE); NOSTOCALES.
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.
RX MEDLINE; 92077441.
RA RYANT D.A., STIREWALT V.L., GLAUSER M., FRANK G., SIDLER W.,

```

```

RA ZUBER H.;
RL GENE 107:91-99(1991).
CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
CC EMBL; M60435; G142102; -.
CC PIR; JS0595; JS0595.
CC KW PHYCOBILISOME; PHOTOSYNTHESIS; MULTIGENE FAMILY.
CC FT INIT_MET 0 0
CC SEQUENCE 252 AA; 29191 MW; 0C1A6468 CRC32;

Query Match 44.2%; Score 68; DB 8; Length 252;
Best Local Similarity 53.8%; Pred. No. 2.71e+00;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 94 yrlvsvnnnyrl 106
||| : :| : |||
QY 1 YRLAIRLNERYRL 13

RESULT 5
ID PYG3_MASLA STANDARD; PRT; 253 AA.
AC P29733;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG3 (L-RC 29.6).
GN CPCG3.
GN MASTIGOCGLADUS LAMINOSUS (FISCHERELLA SP.).
OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
OC CYANOBACTERIA (BLUE-GREEN ALGAE); STIGONEMATATALES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC 7603;
RX MEDLINE; 92249337.
RA GLAUSER M., STIREWALT V.L., BRYANT D.A., SIDLER W., ZUBER H.;
RL EUR. J. BIOCHEM. 205:927-937(1992).
CC -!- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -!- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -!- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
CC EMBL; X59763; G44401; -.
CC PIR; S16060; S16060.
CC DR PIR; S23475; S23475.
CC DR PIR; S23475; S23475.
CC KW PHYCOBILISOME; PHOTOSYNTHESIS; MULTIGENE FAMILY.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC SEQUENCE 253 AA; 29493 MW; 820A835D CRC32;

Query Match 44.2%; Score 68; DB 8; Length 253;
Best Local Similarity 53.8%; Pred. No. 2.71e+00;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 94 yrlvsvnnnyrl 106
||| : :| : |||
QY 1 YRLAIRLNERYRL 13

RESULT 6

```

DE INTEGRIN ALPHA-3 PRECURSOR (GALACTOPROTEIN B3) (GAPB3) (VLA-3 ALPHA
 DE CHAIN) (CD49C).
 GN ITGA3.
 OS CRICETIDAE SP. (HAMSTER).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-FIBROBLAST;
 RX MEDLINE; 90216739.
 RA TSUJI T., YAMAMOTO F.-I., MIURA Y., TAKIO K., TITANI K., PAWAR S.,
 RA OSAWA T., HAKOMORI S.-I.;
 RL J. BIOL. CHEM. 265:7016-7021(1990).
 CC -!- SUBUNIT: DIMER OF AN ALPHA AND BETA CHAINS. THE ALPHA CHAIN IS
 CC COMPOSED OF AN HEAVY AND LIGHT CHAINS LINKED BY A DISULFIDE BOND.
 CC ALPHA-3 ASSOCIATES WITH BETA-1.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: WITH OTHER ALPHA CHAINS FROM THE INTEGRIN FAMILY OF
 CC CELL-SURFACE RECEPTOR.
 DR EMBL; J05281; G304508; -.
 DR PIR; A35761; A35761.
 DR PROSITE; PS00242; INTEGRIN_ALPHA.
 KW CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL; INTEGRIN;
 KW EXTRACELLULAR MATRIX; CYTOSKELETON; REPEAT.
 FT SIGNAL 1 32
 FT CHAIN 33 1051 INTEGRIN ALPHA-3.
 FT CHAIN 33 872 HEAVY CHAIN (POTENTIAL).
 FT CHAIN 876 1051 LIGHT CHAIN (POTENTIAL).
 FT DOMAIN 33 991 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 992 1019 POTENTIAL.
 FT DOMAIN 1020 1051 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 49 461 7 X APPROXIMATE REPEATS.
 FT REPEAT 49 94 I.
 FT REPEAT 120 165 II.
 FT REPEAT 195 227 III.
 FT REPEAT 246 279 IV.
 FT REPEAT 304 345 V.
 FT REPEAT 366 402 VI.
 FT REPEAT 426 461 VII.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CARBOHYD 500 500 POTENTIAL.
 FT CARBOHYD 511 511 POTENTIAL.
 FT CARBOHYD 573 573 POTENTIAL.
 FT CARBOHYD 605 605 POTENTIAL.
 FT CARBOHYD 656 656 POTENTIAL.
 FT CARBOHYD 697 697 POTENTIAL.
 FT CARBOHYD 841 841 POTENTIAL.
 FT CARBOHYD 923 923 POTENTIAL.
 FT CARBOHYD 926 926 POTENTIAL.
 FT CARBOHYD 935 935 POTENTIAL.
 FT CARBOHYD 969 969 POTENTIAL.
 SQ SEQUENCE 1051 AA; 116455 MW; 3363FE0 CRC32;
 Query Match 44.2%; Score 68; DB 5; Length 1051;
 Best Local Similarity 37.5%; Pred. No. 2.71e+00;
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 Db 574 yslplmpdrklgm 589
 QY 1 YRLAIRLNERYLRAIR 16
 RESULT 8
 ID ITA3_HUMAN STANDARD; PRT; 1051 AA.
 AC F26006;
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE INTEGRIN ALPHA-3 PRECURSOR (GALACTOPROTEIN B3) (GAPB3) (VLA-3 ALPHA
 DE CHAIN) (CD49C).
 GN ITGA3.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92011866.
 RA TAKADA Y., MURPHY E., PIL P., CHEN C., GINSBERG M.H., HEMLER M.E.;
 RL J. CELL BIOL. 115:257-266(1991).
 RN [2]
 RP SEQUENCE OF 33-1051 FROM N.A.
 RC TISSUE-FIBROBLAST;
 RX MEDLINE; 91331981.
 RA TSUJI T., HAKOMORI S.-I., OSAWA T.;
 RL J. BIOCHEM. 109:659-665(1991).
 RN [3]
 RP SEQUENCE OF 33-46.
 RX MEDLINE; 87204112.
 RA TAKADA Y., STROMINGER J.L., HEMLER M.E.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:3239-3243(1987).
 CC -!- FUNCTION: VLA-3 ACTS A RECEPTOR FOR FIBRONECTIN, LAMININ AND
 CC COLLAGEN.
 CC -!- SUBUNIT: DIMER OF AN ALPHA AND BETA CHAINS. THE ALPHA CHAIN IS
 CC COMPOSED OF AN HEAVY AND LIGHT CHAINS LINKED BY A DISULFIDE BOND.
 CC ALPHA-3 ASSOCIATES WITH BETA-1.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: WITH OTHER ALPHA CHAINS FROM THE INTEGRIN FAMILY OF
 CC CELL-SURFACE RECEPTOR.
 DR EMBL; M59911; G186497; -.
 DR PIR; JX0161; JX0161.
 DR PROSITE; PS00242; INTEGRIN_ALPHA.
 KW CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL; INTEGRIN;
 KW EXTRACELLULAR MATRIX; CYTOSKELETON; REPEAT.
 FT SIGNAL 1 32
 FT CHAIN 33 1051 INTEGRIN ALPHA-3.
 FT CHAIN 33 872 HEAVY CHAIN (POTENTIAL).
 FT CHAIN 876 1051 LIGHT CHAIN (POTENTIAL).
 FT DOMAIN 33 991 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 992 1019 POTENTIAL.
 FT DOMAIN 1020 1051 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 49 461 7 X APPROXIMATE REPEATS.
 FT REPEAT 49 94 I.
 FT REPEAT 120 165 II.
 FT REPEAT 195 227 III.
 FT REPEAT 246 279 IV.
 FT REPEAT 304 345 V.
 FT REPEAT 366 402 VI.
 FT REPEAT 426 461 VII.
 FT CARBOHYD 86 86 POTENTIAL.
 FT CARBOHYD 107 107 POTENTIAL.
 FT CARBOHYD 265 265 POTENTIAL.
 FT CARBOHYD 500 500 POTENTIAL.
 FT CARBOHYD 511 511 POTENTIAL.
 FT CARBOHYD 573 573 POTENTIAL.
 FT CARBOHYD 605 605 POTENTIAL.
 FT CARBOHYD 656 656 POTENTIAL.
 FT CARBOHYD 697 697 POTENTIAL.
 FT CARBOHYD 841 841 POTENTIAL.
 FT CARBOHYD 857 857 POTENTIAL.
 FT CARBOHYD 926 926 POTENTIAL.
 FT CARBOHYD 935 935 POTENTIAL.
 FT CARBOHYD 969 969 POTENTIAL.
 SQ SEQUENCE 1051 AA; 116612 MW; 1D8A7B0F CRC32;
 Query Match 44.2%; Score 68; DB 5; Length 1051;
 Best Local Similarity 43.8%; Pred. No. 2.71e+00;
 Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 Db 574 yslplmpdrklgm 589
 QY 1 YRLAIRLNERYLRAIR 16
 RESULT 9
 ID REAF_HAEN STANDARD; PRT; 346 AA.

01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NITROGEN REGULATION PROTEIN NR(II) (EC 2.7.3.-).
GLN OR NTRB.
SALMONELLA TYPHIMURUM.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
SEQUENCE FROM N.A.
[1]
STRAIN-LT2;
KUSTU S.G.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
-!- FUNCTION: NTRB ACTS AS A SIGNAL TRANSDUCER WHICH RESPONDS TO THE
NITROGEN LEVEL OF CELL AND MODULATES THE ACTIVITY OF NTRC. IN
NITROGEN LIMITATION NTRB ACTIVATES NTRC BY PHOSPHORYLATING IT,
WHILE IN NITROGEN EXCESS NTRC IS DEPHOSPHORYLATED AND CONSEQUENTLY
INACTIVATED BY NTRB.
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
KINASES.
EMBL; X85104; G728723; -.
STYGENE; SG10569; NTRB.
SENSORY TRANSDUCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;
NITROGEN FIXATION; ATP-BINDING
DOMAIN 116 349 TRANSMITTER DOMAIN (POTENTIAL).
MOD_RES 139 139 PHOSPHORYLATION (AUTO-).
BINDING 329 329 ATP (BY SIMILARITY).
SEQUENCE 349 AA; 38443 MW; EA0E4028 CRC32;
SQ SEQUENCE 349 AA; 38443 MW; EA0E4028 CRC32;
Query Match 42.2%; Score 65; DB 6; Length 349;
Best Local Similarity 47.1%; Pred. No. 7.24e+00;
Matches 8; Conservative 6; Mismatches 2; Indels 1; Gaps

Db 268 fglth-gerylaarl 283
::: |||||
QY 1 YRLAIRLNERYLRL 17

RESULT 12
ID CR72.BACTI STANDARD; PRT; 643 AA.
AC P21256;
DT 01-MAY-1991 (REL. 18, CREATED)
DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
DT 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE 72 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL
DE PROTOXIN).
GN CRYD.
OS BACILLUS THURINGIENSIS (SUBSP. ISRAELENIS).
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89008093.
RA DONOVAN W.P.; DANKOCSIK C.; GILBERT M.P.;
J. BACTERIOL. 170:4732-4738(1988).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF MOSQUITOS.
CC -!- TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOGULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
EMBL; M31737; G142763; -.
DR PIR; A43647; A43647.
KW TOXIN; SPOGULATION.
SQ SEQUENCE 643 AA; 72348 MW; 0C528C2C CRC32;
Query Match 42.2%; Score 65; DB 2; Length 643;
Best Local Similarity 50.0%; Pred. No. 7.24e+00;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps

Db 544 yklirrvpyrlp 557
::: |||||
QY 1 YRLAIRLNERYLRL 14

01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
ADP-HEPTOSE--LPS HEPTOSYLTRANSFERASE II.
REAF OR H1105.
HAEMOPHILUS INFLUENZAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
PASTURELLACEAE.
SEQUENCE FROM N.A.
[1]
STRAIN-RD / KW20;
MEDLINE; 95350630.
RA FLEISCHMANN R.D.; ADAMS M.D.; WHITE O.; CLAYTON R.A.; KIRKNESS E.F.;
KELAVAGE A.R.; BULT C.J.; TOMB J.-F.; DOUGHERTY B.A.; MERRICK J.M.;
MCKENNEY K.; SUTTON G.; FITZHUGH W.; FIELDS C.A.; GOCAYNE J.D.;
SCOTT J.D.; SHIRLEY R.; LIU L.-I.; GLODEK A.; KELLEY J.M.;
WEIDMAN J.F.; PHILLIPS C.A.; SPRIGGS T.; HEDBLOM E.; COTTON M.D.;
UTTERBACK T.R.; HANNA M.C.; NGUYEN D.T.; SAUDEK D.M.; BRANDON R.C.;
FINE L.D.; FRITCHMAN J.L.; FUHRMANN J.L.; GEOGHAGEN N.S.M.;
GNEHM C.L.; MCDONALD L.A.; SMALL K.V.; FRASER C.M.; SMITH H.O.;
RA VENTER J.C.;
SCIENCE 269:496-512(1995).
CC -!- PATHWAY: LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS.
EMBL; L45741; G1008405; -.
DR EMBL; U32790; G926169; -.
KW LIPOPOLYSACCHARIDE BIOSYNTHESIS; TRANSFERASE.
SQ SEQUENCE 346 AA; 38847 MW; 1B4C2E89 CRC32;
Query Match 43.5%; Score 67; DB 8; Length 346;
Best Local Similarity 52.9%; Pred. No. 3.77e+00;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 70 yrlgkslregydmav1 86
::: |||||
QY 1 YRLAIRLNERYLRL 17

RESULT 10
ID YQO5.CAEEL STANDARD; PRT; 424 AA.
AC Q09535;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 48.0 KD PROTEIN F10B5.5 IN CHROMOSOME III.
GN F10B5.5.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA SIMMS M.;
RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SIMILARITY: DISTANTLY RELATED TO THE AAA FAMILY OF ATPASES.
DR EMBL; Z48334; G671827; -.
DR WORMPEP; F10B5.5; CE01547.
KW HYPOTHETICAL PROTEIN; ATP-BINDING.
FT BIND 179 186 ATP (POTENTIAL).
SQ SEQUENCE 424 AA; 48022 MW; 8C8A7686 CRC32;
Query Match 43.5%; Score 67; DB 11; Length 424;
Best Local Similarity 35.3%; Pred. No. 3.77e+00;
Matches 6; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 195 hlslrmadkyskvmle 211
::: |||||
QY 2 RLAIRLNERYLRL 18

RESULT 11
ID NTRB.SALTY STANDARD; PRT; 349 AA.
AC P41788;
DT 01-NOV-1995 (REL. 32, CREATED)

```

RP SEQUENCE FROM N.A.
RX MEDLINE; 90382664.
RA JOHNSONE I.L., MCCABE P.C., GREAVES P., GURR S.J., COLE G.E.,
RW BROW M.A.D., UNKLES S.E., CLUTTERBUCK A.J., KINGHORN J.R., INNIS M.A.;
RL GENE 90-181-192(1990).
CC -1- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).
CC -1- CATALYTIC ACTIVITY: 3 NAD(P)H + NITRITE = 3 NAD(P)(+) + NH(4)OH +
CC H(2)O.
CC -1- SUBUNIT: HOMODIMER.
CC -1- COFACTOR: THIS ENZYME IS A FAD FLAVOPROTEIN THAT ALSO CONTAINS
CC A SIROHEME AND ONE 2FE-2S IRON-SULFUR CENTER.
CC -1- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
CC FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
CC SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
CC EMBL; M58289; G168064; -.
DR PIR; JH0181; JH0181.
DR PROSITE; P500365; NIR_STR.
DR OXIDOREDUCTASE; FAD; FLAVOPROTEIN; IRON-SULFUR; NITRATE ASSIMILATION;
KW HEME; NADP.
KW FT NP_BIND 44 79 FAD (POTENTIAL).
FT NP_BIND 146 176 NAD(P)H (POTENTIAL).
FT METAL 720 720 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 726 726 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 760 760 IRON-SULFUR (2FE-2S) (POTENTIAL).
FT METAL 764 764 IRON-SULFUR (2FE-2S) AND SIROHEME
FT (BY SIMILARITY).
SQ SEQUENCE 1104 AA; 122731 MW; 7A485174 CRC32;

Query Match 41.6%; Score 64; DB 6; Length 1104;
Best Local Similarity 57.1%; Pred. No. 9.99e+00;
Matches 8; Conservative 5; Mismatches 0; Indels 1; Gaps

Db 736 mairleqrvk-slr 748
:||||:|:|:|
QY 3 LAIRLERYRLAIR 16

RESULT 15
ID N358_HUMAN STANDARD; PRT; 3224 AA.
AC P49792;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DE NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD
DE NUCLEOPORIN) (P270).
GN NUP358.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95294031.
RA WU J., MATUNIS M.J., KRAEMER D., BLOBEL G., COUTAVAS E.;
RL J. BIOL. CHEM. 270:14209-14213(1995).
CC -1- FUNCTION: INVOLVED IN TRANSPORT FACTOR (RAN-GTP, KARYOPHERIN)-
CC MEDIATED PROTEIN IMPORT VIA THE F-G REPEAT-CONTAINING DOMAIN
CC WHICH ACTS AS A DOCKING SITE FOR SUBSTRATES. COULD ALSO HAVE
CC ISOMERASE OR CHAPERONE ACTIVITY AND MAY BIND RNA OR DNA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. CYTOPLASMIC FILAMENTS.
CC -1- DOMAIN: CONTAINS MANY X-X-F-G AND X-F-X-F-G REPEATS.
CC -1- SIMILARITY: CONTAINS 4 RANBP1-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS A CYCLOPHILIN-LIKE PPIASE DOMAIN.
DR EMBL; L41840; G857368; -.
DR NUCLEAR PROTEIN; TRANSPORT; REPEAT; ZINC-FINGER; ISOMERASE; ROTAMASE.
KW DOMAIN 1172 1301 RANBP1-LIKE.
FT ZN_FING 1356 1375 C4-TYPE.
FT ZN_FING 1419 1439 C4-TYPE.
FT ZN_FING 1483 1503 C4-TYPE.
FT ZN_FING 1547 1567 C4-TYPE.
FT ZN_FING 1610 1630 C4-TYPE.
FT ZN_FING 1689 1689 C4-TYPE.
FT ZN_FING 1728 1748 C4-TYPE.
FT ZN_FING 1785 1805 C4-TYPE.

```

FT DOMAIN 2013 2142 RANBP1-LIKE.
 FT DOMAIN 2310 2439 RANBP1-LIKE.
 FT DOMAIN 2912 3040 RANBP1-LIKE.
 FT DOMAIN 3063 3224 PPIASE, CYCLOPHILIN-TYPE.
 SQ SEQUENCE 3224 AA; 358214 MW; 113D9513 CRC32;

 Query Match 41.6%; Score 64; DB 6; Length 3224;
 Best Local Similarity 44.4%; Pred. No. 9.99e+00;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

 Db 166 hvnrlrlevyrstkrld 183
 QY 2 RLAINRYRLAIRUNE 19
 ::||| |||::||:

Search completed: Thu May 22 08:34:19 1997
 Job time : 12 secs.

THIS PAGE BLANK (USPTO)

W P S R E H

(TW)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:37:03 1997; MasPar time 2.04 Seconds

Tabular output not generated. 64.216 Million cell updates/sec

Title: >US-08-653-294-36
Description: (1-12) from US08653294.pep
Perfect Score: 98
Sequence: 1 YRLAIRRIALRY 12

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 19.057; Variance 63.971; scale 0.298

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------|-----------|
| 1 | 98 | 100.0 | 12 | 18 | HLA-B2702 84-79-84 pa | 2.34e+03 |
| 2 | 61 | 62.2 | 18 | 13 | Human MHC 1 alpha 1 d | 1.74e+01 |
| 3 | 55 | 56.1 | 911 | 18 | DNA-ligase-III. | 6.61e+01 |
| 4 | 53 | 54.1 | 334 | 5 | Brevibacterium flavum | 1.02e+02 |
| 5 | 53 | 54.1 | 772 | 15 | Enzyme M-11. | 1.02e+02 |
| 6 | 53 | 54.1 | 959 | 14 | Yeast MSH1 protein. | 1.02e+02 |
| 7 | 53 | 54.1 | 971 | 14 | Yeast MSH1 protein w1 | 1.02e+02 |
| 8 | 52 | 53.1 | 20 | 16 | HLA-B2702 CTL modul | 1.27e+02 |
| 9 | 52 | 53.1 | 25 | 18 | HLA-B2702 CTL modul | 1.27e+02 |
| 10 | 52 | 53.1 | 25 | 8 | Peptide fragment of H | 1.27e+02 |
| 11 | 52 | 53.1 | 25 | 16 | HLA-B2702 CTL modul | 1.27e+02 |
| 12 | 52 | 53.1 | 362 | 2 | Sequence of HLA-B51 a | 1.27e+02 |
| 13 | 52 | 53.1 | 362 | 3 | HLA-Bw53 exon. | 1.27e+02 |
| 14 | 52 | 53.1 | 362 | 2 | Sequence of HLA-Bw52 | 1.27e+02 |
| 15 | 52 | 53.1 | 529 | 14 | Alpha 2 subunit of a | 1.27e+02 |
| 16 | 52 | 53.1 | 640 | 15 | Chloroperoxidase | 1.27e+02 |
| 17 | 51 | 52.0 | 263 | 14 | Type I ribosome-inact | 1.57e+02 |
| 18 | 51 | 52.0 | 939 | 1 | pJH1 gene product - b | 1.57e+02 |
| 19 | 51 | 52.0 | 3567 | 8 | eryA region polypepti | 1.57e+02 |
| 20 | 50 | 51.0 | 20 | 18 | HLA-B7.84-75-84 Palin | 1.94e+02 |

21 50 51.0 20 16 R92913 HLA-B7 CTL modulating 1.94e+02
22 50 51.0 224 9 R46556 fbp2, for reverse gen 1.94e+02
23 50 51.0 387 9 R49828 3-acylating enzyme. 1.94e+02
24 50 51.0 4472 19 R97246 Virulence gene cluste 2.40e+02
25 49 50.0 10 18 R95425 HLA-B2702.75-84(D). 2.40e+02
26 49 50.0 10 18 R95413 Alpha1-helix of HLA-B 2.40e+02
27 49 50.0 10 8 R41208 Peptide fragment of C 2.40e+02
28 49 50.0 20 18 R95430 HLA-B2702 84-75T/75-8 2.40e+02
29 49 50.0 20 18 R95428 HLA-B2702 84-75-84 pa 2.40e+02
30 49 50.0 20 1 R95012 Papilloma virus type 2.40e+02
31 49 50.0 25 18 R95412 HLA-B2702.60-84. 2.40e+02
32 49 50.0 25 8 R41205 Peptide fragment of C 2.40e+02
33 49 50.0 25 16 R83090 HLA-B2702 CTL modul 2.40e+02
34 49 50.0 248 2 R07518 Synthetic alpha-trich 2.40e+02
35 49 50.0 248 5 R25573 Mature alpha-Trichosa 2.40e+02
36 49 50.0 255 14 R74181 Type I ribosome-inact 2.40e+02
37 49 50.0 289 2 R07514 Trichosanthin from Tr 2.40e+02
38 49 50.0 289 5 R25572 Trichosanthin from Tr 2.40e+02
39 49 50.0 289 6 R29272 Trichosanthin protein 2.40e+02
40 49 50.0 289 6 R32986 Encodes chinese cucum 2.40e+02
41 49 50.0 289 10 R55129 Alpha-trichosanthin c 2.40e+02
42 49 50.0 428 7 R39284 Murine somatostatin r 2.40e+02
43 49 50.0 4302 19 W00870 Polycystic kidney dis 2.40e+02
44 49 50.0 4339 19 R87539 Polycystic kidney dis 2.40e+02
45 49 50.0 4339 15 R75916 Polycystic kidney dis 2.40e+02

ALIGNMENTS

RESULT 1
ID R95429 standard; peptide; 12 AA.
AC R95429;
DE 12-NOV-1996 (first entry)
DE HLA-B2702 84-79-84 palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PR (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C. Krensky AM;
PI WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
PS R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC the protein p74 from a T-cell lysate. These sequences can be used to isolate
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 12 AA;
Query Match 100.0%; Score 98; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.34e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YRLAIRRLRY 12
 |||||
 QY 1 YRLAIRRLRY 12

RESULT 2

ID R71429 standard; peptide; 18 AA.
 AC R71429;
 DT 12-OCT-1995 (first entry)
 DE Human MHC I alpha 1 domain peptide [Ala81]-Dk-(69-85).
 KW Major histocompatibility complex class I; MHC I; cell receptor;
 KW alpha 1 domain; peptide [Ala81]-Dk-(69-85); interaction modulation;
 KW arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN W09505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI; 95-098577/13.
 PT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71424-R71438 are human major histocompatibility complex class I
 CC (MHC I) alpha 1 domain derived peptides and peptide mutants, they
 CC were used to modulate interactions between MHC I and cell surface
 CC receptors. Via competitive inhibition the peptides diminish the
 CC receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 CC Sequence 18 AA;
 SQ

Query Match 62.2%; Score 61; DB 13; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.74e+01;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 6 frvdlrlalry 17

QY 1 YRLAIRRLRY 12

RESULT 3

ID R95634 standard; Protein; 911 AA.
 AC R95634;
 DT 20-OCT-1996 (first entry)
 DE DNA-ligase-III.
 KW Human; DNA-ligase-III; activated T-lymphocyte; DNA repair;
 KW diagnostic; antibody; immunoassay; antitumor; immunostimulant;
 KW gene therapy; DNA-ligase-III-antagonist.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..67
 FT /note= "Putative signal peptide"
 PN W09614394-A1.
 PD 17-MAY-1996.
 PF 08-NOV-1994; U12922.
 PR 08-NOV-1994; WO-U12922.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Haseltine WA, Wei Y;
 DR WPI; 96-251747/25.
 DN N-PSDB; T27092.
 PT New isolated human DNA ligase III gene - used to develop prods. to
 PT treat, prevent or diagnose DNA disorders such as abnormal cellular
 PT proliferation.
 PS Claim 1; Fig 1; 65pp; English.
 CC This sequence represents human DNA-ligase-III from activated
 CC T-lymphocytes, and includes a putative signal peptide sequence.
 CC DNA-ligase-III is a new protein larger than DNA-ligase-II, and
 CC differs from DNA-ligase-I in repairing single-strand breaks in DNA
 CC efficiently, but not performing blunt-end joining or AMP-dependent

CC relaxation of supercoiled DNA. The DNA, protein and
 CC ligase-specific antibodies against it may be used as diagnostic
 CC agents for cancer, immunosuppression, hypersensitivity to DNA-
 CC damaging agents, etc. A DNA-ligase-antagonist protein may be used
 CC in therapy of these conditions, and DNA encoding the antagonist may
 CC be used in gene therapy.
 SQ Sequence 911 AA;

Query Match 56.1%; Score 55; DB 18; Length 911;
 Best Local Similarity 54.5%; Pred. No. 6.61e+01;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 837 rlaikalelrf 847

QY 2 RLAIRRLRY 12

RESULT 4

ID R28073 standard; Protein; 334 AA.
 AC R28073;
 DT 26-MAR-1993 (first entry)
 DE Brevibacterium flavum MJ-233 biotin synthetase.
 KW bioB; ss.
 OS Brevibacterium flavum MJ-233.
 PN J04278088-A.
 PD 02-OCT-1992.
 PF 04-MAR-1991; 062563.
 PR 04-MAR-1991; JP-062563.
 PA (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
 DR WPI; 92-377571/46.
 DR N-PSDB; Q30766.
 PT DNA fragment contg. corynebacterium biotin synthetase gene -
 PT used to produce biotin synthetase with high efficiency
 PS Claim 6; Page 3; 20pp; Japanese.
 CC The bioB gene from B.flavum MJ-233 can be inserted into a plasmid
 CC and used to transform host microorganisms for increased production
 CC of biotin synthetase.
 CC Sequence 334 AA;
 SQ

Query Match 54.1%; Score 53; DB 5; Length 334;
 Best Local Similarity 41.7%; Pred. No. 1.02e+02;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 265 frlaphptmlrf 276

QY 1 YRLAIRRLRY 12

RESULT 5

ID R79949 standard; Protein; 772 AA.
 AC R79949;
 DT 24-APR-1996 (first entry)
 DE Enzyme M-11.
 KW Enzyme; M-11; Q36; rhizobium; arthrobacter; trehalose;
 KW amylaceous saccharide.
 OS Rhizobium sp. M11.
 FH Key Location/Qualifiers
 FT Misc_difference 502..506
 FT /note= "used for production of probe sequence (T04206)"
 FT Misc_difference 621..625
 FT /note= "used for production of probe sequence (T04207)"
 PN EP-674005-A2.
 PD 27-SEP-1995.
 PF 23-FEB-1995; 301176.
 PR 23-FEB-1994; JP-047956.
 PR 23-FEB-1994; JP-047940.
 PR 06-APR-1994; JP-090728.
 PR 06-APR-1994; JP-090705.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Kubota M, Maruta K, Sugimoto T, Tsusaki K;
 DR WPI; 95-329870/43.
 DR N-PSDB; T04155.
 PT DNA encoding enzyme reduces amylaceous saccharide to produce

PT non-reducing sugar with trehalose end gp. - useful in foods,
 PT cosmetics, pharmaceuticals, etc.
 PS Claim 3; Page 21-22; 178pp; English.
 CC This sequence represents an enzyme that forms a non-reducing sugar with a
 CC trehalose end group, from a reducing anylucose saccharide. The
 CC anylucose saccharides have a degree of glucose polymerisation of 3 or
 CC higher. This sequence was extracted from a liquid culture of Rhizobium
 CC species M-11. By using an oligonucleotide probe based on a fragment of
 CC this sequence, the encoding sequence was obtained. The encoding sequence
 CC was then ligated into a vector and used to produce M-11 in E.coli
 CC transformants. This can also be performed for the DNA encoding enzyme
 CC Q36 (see R04156), which was obtained from Arthrobacter sp. Q36. The
 CC non-reducing sugars produced by the action of these enzymes can be used
 CC in foods, cosmetics, pharmaceuticals and feeds. They are used as
 CC sweeteners, taste and quality improvers, stabilisers, fillers, excipients
 CC and adjuvants. The sugars can also be used as intermediates for
 CC trehalose. The advantages with using these sugars, are that, they are
 CC practically non-reducing (so no browning reaction occurs when they are
 CC heated with proteins), have a mild but good quality sweetness, adequate
 CC viscosity and moisture-retaining properties.
 SQ Sequence 772 AA;

Query Match 54.1%; Score 53; DB 15; Length 772;
 Best Local Similarity 85.7%; Pred. No. 1.02e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 8 yrlqirr 14
 QY 1 YRLAIRR 7
 ||| |||

RESULT 6
 ID R76066 standard; Protein; 959 AA.

AC R76066; 16-JAN-1996 (first entry)
 DT 16-JAN-1996 (first entry)
 DE Yeast MSH1 protein.
 KW Mismatch repair; MSH2; primer; identification; defect; alteration;
 KW cancer; tumour; vaccine.
 OS Saccharomycetes cerevisiae.
 PN W09514085-A2.
 PD 26-MAY-1995.
 PF 17-NOV-1994; U13385.
 PR 17-NOV-1993; US-154792.
 PR 07-DEC-1993; US-163449.
 PR 13-JUN-1994; US-259310.
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 PA (DAND) DANA FARMER CANCER INST.
 PI Fishel R, Kolodner RD, Reenan RAG;
 DR WPI; 95-200377/26.
 DR N-PSDB; Q93913.
 PT Determining alteration in human mismatch repair pathways - used in
 PT the diagnosis, prognosis and therapy of cancers and in screening
 PT assays

PS Example 15; Page 149-153; 256pp; English.
 CC R76066 is the S.cerevisiae mismatch repair pathway protein MSH1. It
 CC is used in the analysis of possible mutations in the human mismatch
 CC repair genes. Defects or alterations in such a gene result in the
 CC accumulation of unstable repeated DNA sequences, a feature of a number
 CC of different cancers. The identification of a defect in the mismatch
 CC repair pathway can be diagnostic of a predisposition to cancer and
 CC prognostic for a particular mammalian cancer e.g colorectal, ovarian,
 CC endometrial (uterine), renal, bladder, skin, rectal and bowel. The
 CC nucleotide sequences and polypeptides of the hMSH2 gene may also be
 CC used for therapy and in vaccines.
 SQ Sequence 959 AA;

Query Match 54.1%; Score 53; DB 14; Length 959;
 Best Local Similarity 50.0%; Pred. No. 1.02e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Db 11 fr-plsrslry 21
 QY 1 YRLAIRRLRY 12
 :|:|:|

RESULT 7
 ID R76070 standard; Protein; 971 AA.
 AC R76070;
 DT 16-JAN-1996 (first entry)
 DE Yeast MSH1 protein with I2CA5 epitope tag.
 KW Mismatch repair; MSH2; primer; identification; defect; alteration;
 KW cancer; tumour; vaccine.
 OS Saccharomycetes cerevisiae.
 PN W09514085-A2.
 PD 26-MAY-1995.
 PF 17-NOV-1994; U13385.
 PR 17-NOV-1993; US-154792.
 PR 07-DEC-1993; US-163449.
 PR 13-JUN-1994; US-259310.
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 PA (DAND) DANA FARMER CANCER INST.
 PI Fishel R, Kolodner RD, Reenan RAG;
 DR WPI; 95-200377/26.
 DR Determining alteration in human mismatch repair pathways - used in
 PT the diagnosis, prognosis and therapy of cancers and in screening
 PT assays

PS Disclosure; Page 167-171; 256pp; English.
 CC R76070 is the S.cerevisiae mismatch repair pathway protein MSH1,
 CC containing the I2CA5 epitope. It is used in the analysis of possible
 CC mutations in the human mismatch repair genes. Defects or alterations
 CC in such a gene result in the accumulation of unstable repeated DNA
 CC sequences, a feature of a number of different cancers. The
 CC identification of a defect in the mismatch repair pathway can be
 CC diagnostic of a predisposition to cancer and prognostic for a
 CC particular mammalian cancer e.g colorectal, ovarian, endometrial
 CC (uterine), renal, bladder, skin, rectal and bowel. The nucleotide
 CC sequences and polypeptides of the hMSH2 gene may also be used for
 CC therapy and in vaccines.
 SQ Sequence 971 AA;

Query Match 54.1%; Score 53; DB 14; Length 971;
 Best Local Similarity 50.0%; Pred. No. 1.02e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Db 11 fr-plsrslry 21
 QY 1 YRLAIRRLRY 12
 :|:|:|

RESULT 8
 ID R92911 standard; peptide; 20 AA.
 AC R92911;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PF 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B7-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83051-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 53.1%; Score 52; DB 16; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Db 1 yrlair-lney 11
||| : ||
QY 1 YRLAIRRALRY 12

RESULT 9
ID R95422 standard; peptide; 25 AA.
AC R95422;
DT 12-NOV-1996 (first entry)
DE HLAB38.6084.
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLAB38.6084. These sequences can be used to isolate the protein p74 from
CC a T-cell lysate. p74 is a T-cell surface membrane protein associated
CC with T-cell activation in mammalian T-cells, and is also immunologically
CC cross reactive with the heat shock protein Hsc70. p74 is found in a
CC limited number of cell types, but is particularly expressed on B and T
CC cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95415), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 18; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Db 15 yrenlr-lalry 25
|| : |||||
QY 1 YRLAIRRALRY 12

RESULT 10
ID R48286 standard; peptide; 25 AA.
AC R48286;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of HLA-B38 antigen.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.

OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Example 13; Page 39; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide is derived from the HLA-B38 antigen and corresponds
CC to the amino acid positions 60-84 of that antigen.
SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 8; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Db 15 yrenlr-lalry 25
|| : |||||
QY 1 YRLAIRRALRY 12

RESULT 11
ID R83093 standard; peptide; 25 AA.
AC R83093;
DT 16-MAY-1996 (first entry)
DE HLAB38 CTL modulating peptide (B38.6084).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLAB38.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 03-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B7S-84 MHC antigen of the recipient
PT host

Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLAB38. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 16; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Db 15 yrenlr-lalry 25
|| : |||||
QY 1 YRLAIRRALRY 12

RESULT 12
ID R03144 standard; protein; 362 AA.

```

AC R03144;
DT 19-MAR-1991 (first entry)
DE Sequence of HLA-B*51 antigen.
KW Probe: HLA class I DNA; immunogen.
OS Homo sapiens.
PN EP-354580-A.
PD 14-FEB-1990.
PF 10-AUG-1989.
PR 11-AUG-1988; JP-200758.
PA (OLYU) Olympus Optical Co., Ltd.
PI Kano K, Takiguchi, M.
DR WPI; 90-046289/07.
PT New DNA for class I human leucocyte antigens and derived probes and
PT transformed cells, useful for DNA typing, as immunogens etc.
PS Disclosure; Pages 12-13; 23pp; English.
CC The HLA class I DNA can be used as a source of probes for use in DNA
CC typing. Transformed cells, which are useful as immunogens, can be
CC obtained by introducing these DNAs into eucaryotic cells.
SQ Sequence 362 AA;

Query Match 53.1%; Score 52; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 98 yrenlr-ialry 108
   || : |||||
Qy 1 YRLAIRRIALRY 12

RESULT 13
ID R12463 standard; Protein; 362 AA.
AC R12463;
DT 29-AUG-1991 (first entry)
DE HLA-B*53 exon.
KW Human leucocyte antigen; probe; major histocompatibility complex;
KW MHC; class I.
OS Homo sapiens.
PN J03112487-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR N-PSDB; Q12114.
PT HLA-B*53 gene, DNA probe and transformant cells - used for
PT immunisation, identifying specificity of antiserum etc.
PS Claim 2; Page 1; 11pp; Japanese.
CC Probes comprising part of the sequence encoding the protein can be
CC used to identify Class I genes. The DNA can be expressed for
CC immunisation of animals and prodn. of monoclonal antibodies
CC specific for the HLA-B*53 antigen. See also J03112485 and
CC J03112486.
SQ Sequence 362 AA;

Query Match 53.1%; Score 52; DB 3; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 98 yrenlr-ialry 108
   || : |||||
Qy 1 YRLAIRRIALRY 12

RESULT 14
ID R03142 standard; protein; 362 AA.
AC R03142;
DT 19-MAR-1991 (first entry)
DE Sequence of HLA-B*52 antigen.
KW Probe: HLA class I DNA; immunogen.
OS Homo sapiens.
PN EP-354580-A.
PD 14-FEB-1990.
PF 10-AUG-1989.

```

```

PR 11-AUG-1988; JP-200758.
PA (OLYU) Olympus Optical Co., Ltd.
PI Kano K, Takiguchi, M.
DR WPI; 90-046289/07.
PT New DNA for class I human leucocyte antigens and derived probes and
PT transformed cells, useful for DNA typing, as immunogens etc.
PS Disclosure; Page 13; 23pp; English.
CC The HLA class I DNA can be used as a source of probes for use in DNA
CC typing. Transformed cells, which are useful as immunogens, can be
CC obtained by introducing these DNAs into eucaryotic cells.
SQ Sequence 362 AA;

Query Match 53.1%; Score 52; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 98 yrenlr-ialry 108
   || : |||||
Qy 1 YRLAIRRIALRY 12

RESULT 15
ID R73966 standard; Protein; 529 AA.
AC R73966;
DT 30-NOV-1995 (first entry)
DE Alpha 2 subunit of a human neuronal nicotinic acetylcholine receptor.
KW Human nNACHr; neuronal nicotinic acetylcholine receptor;
KW neurotransmitter.
OS Homo sapiens.
PN WO9513299-A.
PD 18-MAY-1995.
PF 08-NOV-1994; U12859.
PR 08-NOV-1993; US-149503.
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
PI Elliott KJ, Ellis SB, Harpold MM;
DR WPI; 95-194036/25.
DR N-PSDB; Q90387.
PT New human neuronal nicotinic acetylcholine receptor alpha2 subunit DNA
PT used to develop prods. for detection, diagnosis and therapy and for
PT modulating activity.
PS Disclosure; Page 43-46; 54pp; English.
CC DNA encoding the human nNACHR alpha2 subunit was isolated from a
CC human thalamus tissue cDNA library using corresp. rat cDNA. The
CC insert of one clone obt'd. was ligated with the insert of another
CC clone to generate a full-length alpha 2 subunit cDNA. The DNA can be
CC used to identify function nNACHrs. Cells contg. the DNA can be used
CC for screening to identify cpds. which modulate the activity of human
CC nNACHrs. The human nNACHR alpha 2 subunit can be used to product
CC antibodies which can be used in immunohistochemistry, diagnosis and
CC therapy. The nucleic acids can be used for analysing disease states
CC and creating animal models.
SQ Sequence 529 AA;

Query Match 53.1%; Score 52; DB 14; Length 529;
Best Local Similarity 50.0%; Pred. No. 1.27e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 257 yafvirrlplfy 268
   | : |||:| |
Qy 1 YRLAIRRIALRY 12

Search completed: Thu May 22 08:37:16 1997
Job time : 13 secs.

```

THIS PAGE BLANK (USPTO)

W P S R E A
 (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.

Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.

Distribution rights by Intelligenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:34:36 1997; MasPar time 3.23 Seconds

Tabular output not generated. 176.531 Million cell updates/sec

Title: >US-08-653-294-31

Description: (1-20) from US08653294.pep

Perfect Score: 154

Sequence: 1 YRLAIRLNERYLRLNER 20

Scoring table: PAM 150

Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

pir50
 1:ann1 2:ann2 3:ann3 4:ann4 5:annn1 6:annn2 7:annn3
 8:unann 9:unann5 10:unann6 11:unann7 12:unann8
 13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 28.882; Variance 64.246; scale 0.450

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | ID | Description | Pred. No. |
|------------|-------|---------------|--------|----------------------|-----------|
| 1 | 74 | 48.1 | D49898 | cellobiose phosphotr | 1.85e+00 |
| 2 | 71 | 46.1 | S34613 | 5-exo-hydroxycamphor | 4.43e+00 |
| 3 | 70 | 45.5 | S32869 | outo protein - Erwin | 5.91e+00 |
| 4 | 70 | 45.5 | S19263 | DNA-directed DNA pol | 5.91e+00 |
| 5 | 70 | 45.5 | JDEC22 | DNA-directed DNA pol | 5.91e+00 |
| 6 | 68 | 44.2 | J50595 | rod-core linker poly | 1.04e+01 |
| 7 | 68 | 44.2 | S32475 | rod-core linker poly | 1.04e+01 |
| 8 | 68 | 44.2 | R3ECGL | glnL regulatory prot | 1.04e+01 |
| 9 | 68 | 44.2 | A35761 | cell surface glycopr | 1.04e+01 |
| 10 | 68 | 44.2 | A40021 | integrin VLA-3 alpha | 1.04e+01 |
| 11 | 68 | 44.2 | I55534 | VLA-3 alpha subunit | 1.04e+01 |
| 12 | 67 | 43.5 | G64182 | ADP-heptose-lps hept | 1.38e+01 |
| 13 | 65 | 42.2 | S33023 | nitrogen regulatory | 2.40e+01 |
| 14 | 65 | 42.2 | A33647 | 72k crystal protein | 2.40e+01 |
| 15 | 65 | 42.2 | S62790 | mismatch DNA recogn | 2.40e+01 |
| 16 | 64 | 41.6 | I40586 | hypothetical protein | 3.15e+01 |
| 17 | 64 | 41.6 | LNNTS6 | stylar glycoprotein | 3.15e+01 |
| 18 | 64 | 41.6 | A25047 | beta-glucuronidase | 3.15e+01 |
| 19 | 64 | 41.6 | P50299 | nitrite reductase (N | 3.15e+01 |
| 20 | 64 | 41.6 | JH0181 | nitrite reductase (N | 3.15e+01 |
| 21 | 64 | 41.6 | S58884 | Ran-binding protein | 3.15e+01 |

22 64 41.6 3224 13 A57545 nucleoporin Nup358 - 3.15e+01
 23 63 40.9 115 8 E36811 hypothetical protein 4.13e+01
 24 63 40.9 245 16 S43774 Sli1 protein - Chaco 4.13e+01
 25 63 40.9 261 8 S24418 dmpE protein - Pseud 4.13e+01
 26 63 40.9 485 4 B45343 glycoprotein gp13 pr 4.13e+01
 27 63 40.9 597 14 A30814 development-specific 4.13e+01
 28 63 40.9 649 10 A49512 alpha-amylase (EC 3. 4.13e+01
 29 63 40.9 3165 16 S15010 hypothetical protein 4.13e+01
 30 62 40.3 232 5 S28609 phosphoadenylylsulfa 5.40e+01
 31 62 40.3 558 4 MXXRRT RNA 10 protein - ric 5.40e+01
 32 62 40.3 818 12 S64251 SAP4 protein - yeast 5.40e+01
 33 62 40.3 1155 16 S43275 hypothetical protein 5.40e+01
 34 62 40.3 1176 12 A49848 nitrite reductase - 5.40e+01
 35 62 40.3 1498 12 S53577 Tyb protein - yeast 5.40e+01
 36 62 40.3 1547 12 S69842 Tyb protein - yeast 5.40e+01
 37 61 39.6 108 10 G64386 hypothetical protein 7.04e+01
 38 61 39.6 339 5 S34193 3'-phosphoadenosine 7.04e+01
 39 61 39.6 354 14 B56392 beta-galactoside alp 7.04e+01
 40 61 39.6 372 16 S46344 envelope protein - s 7.04e+01
 41 61 39.6 579 13 B45266 MPL-K protein precu 7.04e+01
 42 61 39.6 587 11 S54061 probable inorganic p 7.04e+01
 43 61 39.6 635 13 R45266 MPL-P protein precu 7.04e+01
 44 61 39.6 928 3 RBHU retinoblastoma-assoc 7.04e+01
 45 61 39.6 1502 4 RBYH1 CYC1/CYP3 transcript 7.04e+01

ALIGNMENTS

RESULT 1

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

RESULT 2

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#contents

#accession

#status

#molecule_type

#residues

#cross-references

#note

SUMMARY

Query Match

Best Local Similarity

Matches

Db

```

dehydrogenase gene on the CAM plasmid of Pseudomonas putida
(ATCC 17453).
#accession S34613
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-361 #label ARA
#experimental_source PpG1; ATCC 17453; CAM plasmid
REFERENCE A29844
#authors Koga, H.; Aramaki, H.; Yamaguchi, E.; Takeuchi, K.; Horiuchi,
T.; Gunsalus, I.C.
#journal J. Bacteriol. (1986) 166:1089-1095
#title camR, a negative regulator locus of the cytochrome P-450-cam
hydroxylase operon.
#cross-references MUID:86223770
#accession A29844
#molecule_type DNA
#residues 1-96, 'RAIIV' #label KOG
#note this sequence has been revised in reference S34613
GENETICS
#gene camD
#genome plasmid
#complex homodimer
#function catalyzes formation of 2,5-diketo-camphane from
5-exo-hydroxycamphor
#classification #superfamily alcohol dehydrogenase; long-chain alcohol
dehydrogenase homology
#keywords NAD; oxidoreductase; zinc
#feature 25-350
#domain long-chain alcohol dehydrogenase homology #label
LADH\
#binding_site zinc, catalytic (Cys, His, Cys) #status
predicted
98,101,104,112 #binding_site zinc, noncatalytic (Cys) #status predicted
#length 361 #molecular-weight 38377 #checksum 992
SUMMARY
Query Match 46.1%; Score 71; DB 5; Length 361;
Best Local Similarity 47.4%; Pred. NO. 4.43e+00;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Db 316 qlaarldrypladitqr 334
:||||:||||:|
QY 2 RLAIRLNERYRLAIRLN 20

RESULT 3
ENTRY #type complete
TITLE outO protein - Erwinia carotovora subsp. carotovora
ORGANISM #formal_name Erwinia carotovora subsp. carotovora
DATE 08-Dec-1993 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996
ACCESSIONS S32869; S31758
REFERENCE S32857
#authors Reeves, P.J.; Whitcombe, D.; Wharam, S.; Gibson, M.; Allison,
G.; Bunce, N.; Barallion, R.; Douglas, P.; Mulholland, V.;
Stevens, S.; Walker, D.; Salmond, G.P.C.
#journal Mol. Microbiol. (1993) 8:443-456
#title Molecular cloning and characterization of 13 out genes from
Erwinia carotovora subspecies carotovora: genes encoding
members of a general secretion pathway (GSP) widespread in
gram-negative bacteria.
#accession S32869
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-279 #label REE
#cross-references EMBL:X70049
#note the nucleotide sequence was submitted to the EMBL Data
Library, December 1992
GENETICS
#gene outO
#start_codon GTG
#summary #length 279 #molecular-weight 31131 #checksum 5854

```

```

Query Match 45.5%; Score 70; DB 9; Length 279;
Best Local Similarity 50.0%; Pred. NO. 5.91e+00;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Db 35 yrlpimlerrwrqdiele 52
||||:| | | |
QY 1 YRLAIRLNERYLAIRLN 18

RESULT 4
ENTRY #type complete
TITLE DNA-directed DNA polymerase (EC 2.7.7.7) (version 1) -
Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
15-Jun-1996
ACCESSIONS S19263; S12820; B36236; JT0943; JU0325
REFERENCE S19263
#authors Chen, H.
#submission submitted to the EMBL Data Library, June 1990
#accession S19263
#molecule_type DNA
#residues 1-768 #label CHE
#cross-references EMBL:M35371
REFERENCE S12820
#authors Chen, H.; Lawrence, C.B.; Bryan, S.K.; Moses, R.E.
#journal Nucleic Acids Res. (1990) 18:7185-7186
#title Aphidicolin inhibits DNA polymerase II of Escherichia coli,
an alpha-like DNA polymerase.
#cross-references MUID:91088346
#accession S12820
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 90-768 #label CHE2
#cross-references EMBL:M35371
REFERENCE A36236
#authors Chen, H.; Sun, Y.; Stark, T.; Beattie, W.; Moses, R.E.
#journal DNA Cell Biol. (1990) 9:631-635
#title Nucleotide sequence and deletion analysis of the polB gene of
Escherichia coli.
#cross-references MUID:91083835
#accession B36236
#status preliminary
#molecule_type DNA
#residues 'V', 2-768 #label CH2
#cross-references GB:M35371
GENETICS
#gene polB
#map_position 2 min
#start_codon GTG
#classification #superfamily DNA-directed DNA polymerase II
#keywords DNA synthesis; nucleotidyltransferase
#summary #length 768 #molecular-weight 87931 #checksum 4470

Query Match 45.5%; Score 70; DB 5; Length 768;
Best Local Similarity 50.0%; Pred. NO. 5.91e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Db 231 rmlqkhaeryrlpirl 246
|:|:| | | | | |
QY 2 RLAIRLNERYRLAIRL 17

RESULT 5
ENTRY #type complete
TITLE JDEC22 DNA-directed DNA polymerase (EC 2.7.7.7) II (version 2) -
Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
19-Oct-1995
ACCESSIONS S15943; S19262; S40576; JQ0780; A38840; JQ0688
REFERENCE S15943
#authors Iwasaki, H.; Ishino, Y.; Toh, H.; Nakata, A.; Shinagawa, H.

```

```

#journal Mol. Gen. Genet. (1991) 226:24-33
#title Escherichia coli DNA polymerase II is homologous to
#cross-references MUID:91238699
#accession SI5943
##molecule_type DNA
##residues 1-783 ##label IWA
##cross-references EMBL:X54847
#accession SI9262
##molecule_type protein
##residues 2-9 ##label IWA2
REFERENCE S40531
#authors Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.;
#submission Fujita, N.; Isono, K.; Mizobuchi, K.; Nakata, A.
#description submitted to the EMBL Data Library, December 1992
#description Systematic sequencing of the Escherichia coli genome:
#analysis of the 0-2.4min region.
#accession S40576
##status preliminary
##molecule_type DNA
##residues 'V', 2-783 ##label YUR
##cross-references EMBL:D10483
REFERENCE JQ0780
#authors Bonner, C.A.; Hays, S.; McEntee, K.; Goodman, M.F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7663-7667
#title DNA polymerase II is encoded by the DNA damage-inducible dinA
#cross-references MUID:91017565
#accession JQ0780
##molecule_type DNA
##residues 1-256, 'DD', 259-271, 'G', 273-458 ##label BON
##cross-references GB:M37727
#accession A38840
##molecule_type protein
##residues 2-9, 'XQ', 12-21, 'H', 23, 'X', 25-28 ##label B02
GENETICS
#gene polB
#map_position 2 min
#start_codon GTG
CLASSIFICATION #superfamily DNA-directed DNA polymerase II
KEYWORDS DNA synthesis; nucleotidyltransferase
FEATURE 2-783
#product DNA-directed DNA polymerase II #status
#experimental #label MAT
SUMMARY #length 783 #molecular-weight 90052 #checksum 2286
Query Match 45.5%; Score 70; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 5.91e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Db 231 rmlqkhaeryrlplrl 246
| : : |||||:|
QY 2 RLAIRLNERYLRL 17
RESULT 6
ENTRY JS0595 #type complete
TITLE rod-core linker polypeptide cpcG4 - Anabaena sp. (PCC 7120)
ALTERNATE_NAMES #formal_name Anabaena sp.
ORGANISM #formal_name Anabaena sp.
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
ACCESSION JS0595; PS0243
REFERENCE JS0592
#authors Bryant, D.A.; Stirewalt, V.L.; Glauser, M.; Frank, G.;
#journal Sieder, W.; Zuber, H.
#title Gene (1991) 107:91-99
#description A small multigene family encodes the rod-core linker
#cross-references MUID:92077441
#accession JS0595
##molecule_type DNA
##residues 1-253 ##label GRY
##cross-references GB:M80435

```

```

#accession PS0243
##molecule_type protein
##residues 2-23 ##label GRY1
COMMENT Linker polypeptides determine the positions of phycobiliproteins
within the phycobilisome structure.
GENETICS
#gene cpcG4
#feature 2-253
#product rod-core linker polypeptide cpcG4 #status
#experimental #label MAT
SUMMARY #length 253 #molecular-weight 29323 #checksum 5904
Query Match 44.2%; Score 68; DB 9; Length 253;
Best Local Similarity 53.8%; Pred. No. 1.04e+01;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 95 yrlvsvnnnyrl 107
| : : |||
QY 1 YRLAIRLNERYLRL 13
RESULT 7
ENTRY S23475 #type complete
TITLE rod-core linker polypeptide cpcG3 - Fischerella sp.
ALTERNATE_NAMES #formal_name Fischerella sp.
ORGANISM #formal_name Fischerella sp.
DATE 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
ACCESSION S23475; S16060
REFERENCE S23472
#authors Glauser, M.; Stirewalt, V.L.; Bryant, D.A.; Sieder, W.;
#journal Zuber, H.
#title Eur. J. Biochem. (1992) 205:927-937
#description Structure of the genes encoding the rod-core linker
#cross-references EMBL:X59763
#note the source is designated as Mastigocladus laminosus and
functional aspects of the
polypeptides of Mastigocladus laminosus phycobilisomes and
phycobiliprotein/linker-polypeptide interactions.
#accession S23475
##molecule_type DNA
##residues 1-254 ##label GLA
##cross-references EMBL:X59763
GENETICS #note
#gene cpcG3
SUMMARY #length 254 #molecular-weight 29624 #checksum 7870
Query Match 44.2%; Score 68; DB 9; Length 254;
Best Local Similarity 53.8%; Pred. No. 1.04e+01;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 95 yrlvsvnnnyrl 107
| : : |||
QY 1 YRLAIRLNERYLRL 13
RESULT 8
ENTRY RGEGL #type complete
TITLE glnL regulatory protein II - Escherichia coli
ALTERNATE_NAMES ntrB regulatory protein
ORGANISM #formal_name Escherichia coli
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
ACCESSION A30377; S40814; B23970; Q00553
REFERENCE A30377
#authors Miranda-Rios, J.; Sanchez-Pescador, R.; Urdea, M.;
#journal Covarrubias, A.A.
#title Nucleic Acids Res. (1987) 15:2757-2770
#description The complete nucleotide sequence of the glnALG operon of
Escherichia coli K12.
#cross-references MUID:87174797
#accession A30377
##molecule_type DNA
##residues 1-349 ##label MIR
REFERENCE S40802

```

#authors Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
 #journal Nucleic Acids Res. (1993) 21:3391-3398
 #title Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.

#accession S40814

##status preliminary; nucleic acid sequence not shown;

translation not shown

##molecule_type DNA

##residues 1-349 #label PLU

##cross-references EMBL:L1201

##note the nucleotide sequence was submitted to the EMBL Data Library, October 1993

REFERENCE

#authors A91533

#journal Rocha, M.; Vazquez, M.; Garciaarrubio, A.; Covarrubias, A.A.

#title Gene (1985) 37:91-99

#title Nucleotide sequence of the glnA-glnL intercistronic region of Escherichia coli.

#cross-references MUID:86031370

#accession B23970

##molecule_type DNA

##residues 1-24 #label ROC

GENETICS

#gene glnL; ntrB

#map_position 87 min

FUNCTION

#description acts as a signal transducer that responds to the nitrogen level of the cell and modulates the activity of glnG protein; at a low nitrogen level, glnG protein is activated through phosphorylation; at a high nitrogen level, it is deactivated through dephosphorylation
 #superfamily glnL regulatory protein II
 #ATP binding; regulatory protein; signal transduction
 #length 349 #molecular-weight 38556 #checksum 8402

CLASSIFICATION

KEYWORDS

SUMMARY

Query Match 44.2%; Score 68; DB 4; Length 349;

Best Local Similarity 44.4%; Pred. No. 1.04e+01;

Matches 8; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Db 268 fqtlb-gerylaaxid 284

YRLAIRLNERYLRLN 18

RESULT 9

ENTRY

A35761 #type complete

cell surface glycoprotein b3 precursor - golden hamster

#formal_name Mesocricetus auratus common_name golden hamster

12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change

31-Dec-1993

ACCESSIONS A35761

REFERENCE A35761

#authors Tsuji, T.; Yamamoto, F.; Miura, Y.; Takio, K.; Titani, K.;

Pawar, S.; Osawa, T.; Hakomori, S.

J. Biol. Chem. (1990) 265:7016-7021

#journal Characterization through cDNA cloning of galactoprotein b3

(Gap b3), a cell surface membrane glycoprotein showing

enhanced expression on oncogenic transformation.

Identification of Gap b3 as a member of the integrin

superfamily.

#cross-references MUID:90216739

#accession A35761

##status preliminary

##molecule_type mRNA

##residues 1-1051 #label TSU

##cross-references GB:J05281

KEYWORDS

SUMMARY

#length 1051 #molecular-weight 116455 #checksum 9974

Query Match 44.2%; Score 68; DB 14; Length 1051;

Best Local Similarity 37.5%; Pred. No. 1.04e+01;

Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db . 574 yslplmpdrklmgr 589

QY 1 YRLAIRLNERYLRLN 16

RESULT 10

ENTRY

A40021 #type complete

integrin VLA-3 alpha-3 chain precursor - human

fusion regulatory protein FRP2; galactoprotein b3; very late

antigen-3 alpha chain

#formal_name Homo sapiens #common_name man

17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change

06-Sep-1996

ACCESSIONS A40021; JX0161; C28018; S44356

REFERENCE A40021

#authors Takada, Y.; Murphy, E.; Pil, P.; Chen, C.; Ginsberg, M.H.;

Hemler, M.E.

J. Cell Biol. (1991) 115:257-266

#journal Molecular cloning and expression of the cDNA for alpha-3

subunit of human alpha-3beta-1 (VLA-3), an integrin-

receptor for fibronectin, laminin, and collagen.

#cross-references MUID:92011866

#accession A40021

##molecule_type mRNA

##residues 1-1051 #label TAK

##cross-references GB:M59911

REFERENCE JX0161

#authors Tsuji, T.; Hakomori, S.; Osawa, T.

J. Biochem. (1991) 109:659-665

#journal Identification of human galactoprotein b3, an oncogenic

transformation-induced membrane glycoprotein, as VLA-3

alpha subunit: The primary structure of human integrin

alpha 3.

#cross-references MUID:91331981

#accession JX0161

##molecule_type mRNA

##residues 33-1051 #label TSU

REFERENCE A94151

#authors Takada, Y.; Strominger, J.L.; Hemler, M.E.

Proc. Natl. Acad. Sci. U.S.A. (1987) 84:3239-3243

#journal The very late antigen family of heterodimers is part of a

superfamily of molecules involved in adhesion and

embryogenesis.

#cross-references MUID:87204112

#accession C28018

##molecule_type protein

##residues 33-46 #label TAK

REFERENCE S44356

#authors Ohta, H.; Tsurudome, M.; Matsumura, H.; Koga, Y.; Morikawa,

S.; Kawano, M.; Kusugawa, S.; Komada, H.; Nishio, M.; Ito,

Y.

EMBO J. (1994) 13:2044-2055

#journal Molecular and biological characterization of fusion

regulatory proteins (FRPs): anti-FRP mAbs induced

HIV-mediated cell fusion via an integrin system.

#accession S44356

##status preliminary

##molecule_type protein

##residues 33-43, 'X', 45-49 #label OHT

GENETICS

#gene

GDB:ITGA3

##cross-references GDB:128972

cell adhesion; duplication; glycoprotein; heterodimer; metal

binding; transmembrane protein

FEATURE

1-32

33-871

##domain signal sequence #status predicted #label SIG\

#product integrin alpha-3 heavy chain #status predicted

#label CHN

#region calcium/magnesium binding #status predicted\

#region calcium/magnesium binding #status predicted\

#region calcium/magnesium binding #status predicted\

#region calcium/magnesium binding #status predicted\

#product integrin alpha-3 light chain #status predicted

```

##cross-references GB:I42023; TIGR:HL105
##note      named as homolog to a protein from Escherichia coli
SUMMARY     #length 346 #molecular-weight 38847 #checksum 9828

Query Match      43.5%; Score 67; DB 9; Length 346;
Best Local Similarity 52.9%; Pred. No. 1.38e+01;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 70 yrigkslregydmavil 86
    |||  | | | : | | |
Qy 1 YRLAIRLNEYRLAIRL 17

RESULT 13
ENTRY      S53023 #type complete
TITLE      nitrogen regulatory protein B - Salmonella typhimurium
ORGANISM   #formal_name Salmonella typhimurium
DATE       08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
          03-May-1996
ACCESSIONS S53023
REFERENCE   S53022
#authors   Kustu, S.G.
#submission submitted to the EMBL Data Library, March 1995
#accession S53023
##status   preliminary
##molecule_type DNA
##residues 1-349 #label KUS
##cross-references EMBL:X85104
CLASSIFICATION #superfamily glnL regulatory protein II
SUMMARY      #length 349 #molecular-weight 38443 #checksum 6851

Query Match      42.2%; Score 65; DB 7; Length 349;
Best Local Similarity 47.1%; Pred. No. 2.40e+01;
Matches 8; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

Db 268 fqtlh-geryrlaarl 283
    : | : : | | | | | :
Qy 1 YRLAIRLNEYRLAIRL 17

RESULT 14
ENTRY      A43647 #type complete
TITLE      72K crystalal protein - Bacillus thuringiensis subsp.
          israelensis
ORGANISM   #formal_name Bacillus thuringiensis subsp. israelensis
DATE       03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
          01-Mar-1996
ACCESSIONS A43647; A32256
REFERENCE   A43647
#authors   Donovan, W.P.; Dankocsik, C.; Gilbert, M.P.
#journal   J. Bacteriol. (1988) 170:4732-4738
#title     Molecular characterization of a gene encoding a 72-kilodalton
          mosquito-toxic crystal protein from Bacillus thuringiensis
          subsp. israelensis.
#accession A43647
##status   preliminary
##molecule_type DNA
##residues 1-643 #label DON
##cross-references GB:M31737
REFERENCE   A32256
#authors   Adams, L.F.; Visick, J.E.; Whiteley, H.R.
#journal   J. Bacteriol. (1989) 171:521-530
#title     A 20-kilodalton protein is required for efficient production
          of the Bacillus thuringiensis subsp. israelensis
          27-kilodalton crystal protein in Escherichia coli.
#cross-references MVID:89123065
#accession A32256
##status   preliminary; not compared with conceptual translation
##molecule_type DNA
##residues 566-643 #label ADA

GENETICS
#gene      cryd
SUMMARY    #length 643 #molecular-weight 72348 #checksum 6237

```

Query Match 42.2%; Score 65; DB 10; Length 643;
 Best Local Similarity 50.0%; Pred. No. 2.40e+01;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 544 ykllirrvprip 557
 | : | | : | | :
 QY 1 YRLAIRLNERYRLA 14

RESULT 15
 ENTRY S62790 #type complete
 TITLE mismatch DNA recognition protein mutS - Thermus aquaticus
 (fragment)
 ORGANISM #formal_name Thermus aquaticus
 DATE 23-Aug-1996 #sequence_revision 23-Aug-1996 #text_change
 23-Aug-1996
 ACCESSIONS S62790
 REFERENCE S62790
 #authors Takamatsu, S.; Kato, R.; Kuramitsu, S.
 #journal Nucleic Acids Res. (1996) 24:640-647
 #title Mismatch DNA recognition protein from an extremely
 thermophilic bacterium, Thermus thermophilus HB8.
 #accession S62790
 ##status preliminary
 ##residues 1-818 #label TAK
 ##cross-references EMBL:D63810
 SUMMARY #length 818 #molecular-weight 91322 #checksum 6755

Query Match 42.2%; Score 65; DB 16; Length 818;
 Best Local Similarity 52.9%; Pred. No. 2.40e+01;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 331 rllfrladrlerlatrle 347
 | : | | : | | :
 QY 2 RLAIRLNERYRLAIRLN 18

Search completed: Thu May 22 08:35:05 1997
 Job time : 29 secs.

AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*2702 84-75-84 palindromic.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1993.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*2702 84-75-84 palindromic. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B*2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 CC Sequence 20 AA;

Query Match 53.9%; Score 83; DB 18; Length 20;
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 Db 1 yrlairlner-renlralr 19
 QY 1 YRLAIRLNERYRLAIRLNER 20

RESULT 3
 ID R92907 standard; peptide; 20 AA.
 AC R92907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 53.9%; Score 83; DB 16; Length 20;
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 Db 1 yrlairlner-renlralr 19
 QY 1 YRLAIRLNERYRLAIRLNER 20

RESULT 4
 ID R92909 standard; peptide; 20 AA.
 AC R92909;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 50.6%; Score 78; DB 16; Length 20;
 Best Local Similarity 65.0%; Pred. No. 3.49e+00;
 Matches 13; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
 Db 1 yrlairlner-renlralr 19
 QY 1 YRLAIRLNERYRLAIRLNER 20

RESULT 5
 ID R92908 standard; peptide; 20 AA.
 AC R92908;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 49.4%; Score 76; DB 16; Length 20;
 Best Local Similarity 60.0%; Pred. No. 5.10e+00;
 Matches 12; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

DB 1 yrlatrlner-renlralr 19
 QY 1 YRLAIRLNERYLRLRLNER 20
 ||||| ||||| | : |

RESULT 6
 ID R95430 standard; peptide; 20 AA.
 AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*2702 84-75T/75-84T palindrome.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. These sequences can be used to
 CC HLA-B*2702 84-75T/75-84T palindromes. These sequences can be used to
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B*2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B*2702.60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.
 CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 46.8%; Score 72; DB 18; Length 20;
 Best Local Similarity 72.2%; Pred. No. 1.09e+01;

Matches 13; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

DB 1 yrlatrlnerrenlralr 18
 QY 1 YRLAIRLNER-YRLRLNER 17
 ||||| ||||| | : |

RESULT 7
 ID R92910 standard; peptide; 20 AA.
 AC R92910;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 46.1%; Score 71; DB 16; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.31e+01;
 Matches 12; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

DB 1 yrlatrlnerrenlralr 19
 QY 1 YRLAIRLNERYLRLRLNER 20
 ||||| ||||| | : |

RESULT 8
 ID R24441 standard; Protein; 783 AA.
 AC R24441;
 DT 08-DEC-1992 (first entry)
 DE E. coli DNA polymerase II.
 KW Expression plasmid; industrial production.
 OS Escherichia coli.
 PN J04141088-A.
 PD 14-MAY-1992.
 PF 02-OCT-1990; 263125.
 PR 02-OCT-1990; JP-263125.
 PA (TAKI) TAKARA SHUZO CO LTD.
 DR WPI: 92-212759/26.
 DR N-PSDB: 025440.
 PT Novel Escherichia coli DNA polymerase II - contains specific
 PT aminoacid sequence, obcd. by culturing DNA of recombinant plasmid
 PT introduced transformant etc.
 PS Disclosure; Fig 1; 8pp; Japanese.
 CC The sequence is E. coli DNA polymerase II. The DNA encoding this
 CC sequence can be introduced into expression plasmids which can then be
 CC used to transform cells such that the new polymerase can be collected
 CC from the culture on an industrial scale.
 SQ Sequence 783 AA;

Query Match 45.5%; Score 70; DB 5; Length 783;
 Best Local Similarity 50.0%; Pred. No. 1.58e+01;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 231 rmlqkhaeryrlprl 246
 QY 2 RLAIRLNERYRLAIRL 17

RESULT 9
 ID R70841 standard; Protein; 783 AA.
 AC R70841;
 DT 31-AUG-1995 (first entry)
 DE E. coli polymerase-II.
 KW DNA-polymerase; DNA sequencing; 3'-5' exonuclease; replication;
 KW enzyme engineering; protein engineering; mutagenesis.
 OS Escherichia coli.
 PN WO9504162-A.
 PD 09-FEB-1995.
 PF 01-AUG-1994; U08610.
 PR 02-AUG-1993; US-101593.
 PA (UYAL-) UNIV ALBERTA.
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 PI Goodman MF, Reha-Krantz LJ;
 DR WPI; 95-082243/11.
 DR N-PSDB; Q85427.
 PT Variant DNA polymerase(s) for DNA sequencing - having reduced
 PT 3'-5' exonuclease activity or having enhanced DNA replication
 PT activity
 PS Disclosure; Page 28-31; 45pp; English.
 CC The E. coli DNA-polymerase-II (given in R70841) may be engineered
 CC by mutagenesis of the encoding DNA (Q85427) for use with novel
 CC combinations of deoxynucleotides and chain-terminating
 CC nucleotides in new DNA sequencing protocols. Variants pref.
 CC include D156A and/or E158A mutations.
 SQ Sequence 783 AA;

Query Match 45.5%; Score 70; DB 13; Length 783;
 Best Local Similarity 50.0%; Pred. No. 1.58e+01;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 231 rmlqkhaeryrlprl 246
 QY 2 RLAIRLNERYRLAIRL 17

RESULT 10
 ID R14118 standard; Protein; 1019 AA.
 AC R14118;
 DT 10-DEC-1991 (first entry)
 DE Human GAP b3 protein.
 KW Galactoprotein b3; carcinoma; cancer; tumour.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified -site 54
 FT /label= N-glycosylation
 FT Modified -site 85
 FT /label= N-glycosylation
 FT Binding-site 136..144
 FT /label= divalent cation binding site
 FT Binding-site 209..217
 FT /label= divalent cation binding site
 FT Modified -site 233
 FT /label= N-glycosylation
 FT Binding-site 283..291
 FT /label= divalent cation binding site
 FT Binding-site 346..354
 FT /label= divalent cation binding site
 FT Binding-site 407..415
 FT /label= divalent cation binding site
 FT Modified -site 468
 FT /label= N-glycosylation
 FT Modified -site 479

FT /label= N-glycosylation
 FT Modified -site 541
 FT /label= N-glycosylation
 FT Modified -site 573
 FT /label= N-glycosylation
 FT Modified -site 624
 FT /label= N-glycosylation
 FT Modified -site 665
 FT /label= N-glycosylation
 FT Modified -site 809
 FT /label= N-glycosylation
 FT Modified -site 825
 FT /label= N-glycosylation
 FT Cleavage-site 840..841
 FT Modified -site 894
 FT /label= N-glycosylation
 FT Modified -site 903
 FT /label= N-glycosylation
 FT Modified -site 937
 FT /label= N-glycosylation
 FT Domain 960..987
 FT /label= transmembrane domain
 PN WO9113983-A.
 PD 19-SEP-1991.
 PF 08-APR-1991; U01606.
 PR 12-MAR-1990; US-491910.
 PA (BIOM-) BIOMEMBRANE INST.
 PI Tsuji T, Yamamoto F, Hakomori S;
 DR WPI; 91-295637/40.
 DR N-PSDB; Q13822.
 PT DNA sequences encoding galactoprotein b3 - produced using DNA
 PT constructs also antibodies to Gap b3 used to detect tumours that
 PT result in elevated expression of protein.
 PS Disclosure; Fig 6; 46pp; English.
 CC The sequence was deduced from 3 overlapping clones isolated from
 CC a human T24 cell line cDNA library. The DNA can be used to express
 CC the Gap b3 protein which is a transformation-dependent cell surface
 CC glycoprotein. The C-terminal 32 AA segment is likely to constitute
 CC the cytoplasmic domain with the longer 959 AA residue segment
 CC forming a glycosylated extracellular domain. The N-terminal region
 CC has seven homologous repeats, three of which include the putative
 CC metal binding sequences. Each repeat consists of a long (21-28 AA)
 CC stretch followed by a short (5 AA) stretch. The alignment of
 CC glycine and hydrophobic residues in each repeat shows a similar
 CC pattern, especially the presence of XXXGAP (X= a hydrophobic AA) at
 CC the end of most of the longer stretches (except for the 2nd and 7th
 CC repeats. The protein may be used to produce antibodies and these,
 CC or the DNA sequences, can be used to detect and quantify levels of
 CC Gap b3 protein or mRNA in biological samples. A high level of the
 CC protein is indicative of certain cancers.
 CC See also R14117.
 SQ Sequence 1019 AA;

Query Match 44.2%; Score 68; DB 3; Length 1019;
 Best Local Similarity 43.8%; Pred. No. 2.29e+01;
 Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 542 yslplrmprlprl 557
 QY 1 YRLAIRLNERYLRLAIR 16

RESULT 11
 ID R14117 standard; Protein; 1051 AA.
 AC R14117;
 DT 10-DEC-1991 (first entry)
 DE Hamster GAP b3 protein.
 KW Galactoprotein b3; carcinoma; cancer; tumour.
 OS Cricetulus griseus.
 FH Key Location/Qualifiers
 FT Peptide 1..32
 FT /label= signal sequence
 FT Cleavage-site 32..33

FT Protein 33..1051
 FT /label= mature Gap b3
 FT Peptide 33..50
 FT /note= "confirmed by Edman degradation"
 FT Binding-site 315 323
 FT /label= divalent cation binding site
 FT Binding-site 346..354
 FT /label= divalent cation binding site
 FT Binding-site 406..415
 FT /label= divalent cation binding site
 FT Modified-site 468
 FT /label= N-glycosylation
 FT Modified-site 479
 FT /label= N-glycosylation
 FT Modified-site 541
 FT /label= N-glycosylation
 FT Peptide 544..572
 FT /note= "confirmed by Edman degradation"
 FT Modified-site 573
 FT /label= N-glycosylation
 FT Modified-site 624
 FT /label= N-glycosylation
 FT Modified-site 665
 FT /label= N-glycosylation
 FT Peptide 755..784
 FT /note= "confirmed by Edman degradation"
 FT Modified-site 809
 FT /label= N-glycosylation
 FT Cleavage-site 840..841
 FT Modified-site 891
 FT /label= N-glycosylation
 FT Modified-site 902
 FT /label= N-glycosylation
 FT Modified-site 937
 FT /label= N-glycosylation
 FT Domain 960..987
 FT /label= transmembrane domain
 PN W09113983-A.
 PD 19-SEP-1991.
 PF 08-APR-1991; U01606.
 PR 12-MAR-1990; US-491910.
 PA (BION-) BIOMEMBRANE INST.
 PI Tsuji T, Yamamoto F, Hakomori S;
 DR WPI: 91-295637/40.
 DR N-PSDB; Q13821.
 DT DNA sequences encoding galactoprotein b3 - produced using DNA
 PT constructs also antibodies to Gap b3 used to detect tumours that
 PT result in elevated expression of protein.
 PS Disclosure; Fig 4; 46pp; English.
 CC The sequence was deduced from 3 overlapping clones isolated from
 CC a hamster Nilp cDNA library. The DNA can be used to express the
 CC Gap b3 protein which is a transformation-dependent cell surface
 CC glycoprotein. The C-terminal 32 AA segment is likely to constitute
 CC the cytoplasmic domain with the longer 959 AA residue segment
 CC forming a glycosylated extracellular domain. The protein may be
 CC used to produce antibodies and these, or the DNA sequences, can be
 CC used to detect and quantify levels of Gap b3 protein or mRNA in
 CC biological samples. A high level of the protein is indicative of
 CC certain cancers.
 CC See also R14118.
 SQ Sequence 1051 AA;

Query Match 44.2%; Score 68; DB 3; Length 1051;
 Best Local Similarity 37.5%; Pred. No. 2.29e+01;
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 574 yslpmpdrklgm 589
 |:::|:|:|:|
 QY 1 YRLAIRLNERVLAIR 16

RESULT 12
 ID R97735 standard; Protein; 643 AA.

AC R97735;
 DT 19-NOV-1996 (first entry)
 DE Bacillus thuringiensis ssp. israelensis CryIVD protein.
 KW CryIVD; toxic protein; crystal toxin; expression construct;
 KW transformed cyanobacteria; phycocyanin beta; cpCB; promoter;
 KW insecticide; dipteran larvae; mosquito; blackfly.
 OS Bacillus thuringiensis.
 PN US551897-A.
 PD 21-MAY-1996.
 PF 04-MAY-1992; 877876.
 PR 04-MAY-1992; US-877876.
 PR 28-JAN-1994; US-188581.
 PA (UYNE-) UNIV MEMPHIS STATE.
 PI Murphy RC, Stevens SE;
 DR WPI: 96-259063/26.
 DR N-PSDB; T29774.
 DT New DNA construct for expressing cryIV D protein in cyanobacteria -
 PT under control of a phycocyanin beta promoter, useful for control of
 PT dipteran larvae in water
 PS Example 1; Columns 9-14; 20pp; English.
 CC The present sequence is the B. thuringiensis ssp. israelensis CryIVD
 CC toxic protein, the DNA of which was used in the prepn. of a claimed
 CC DNA construct for the expression of CryIVD in cyanobacteria,
 CC comprising the CryIVD DNA under the control of phycocyanin beta
 CC (cpCB) promoter. Cyanobacteria (which may be adapted for growth in
 CC fresh or brackish water) transformed with the construct can be used
 CC as insecticides for controlling dipteran larvae, esp. those of
 CC mosquitoes and blackflies, that live in water. The percentage of
 CC Culex pipiens (mosquito) larvae surviving after 4 days with
 CC cyanobacteria transformed with the claimed DNA construct as their
 CC only food source was 51 %, compared to 94 % for those fed with
 CC cyanobacteria transformed with an empty plasmid. In the
 CC cyanobacteria, CryIVD is efficiently expressed under the control of
 CC the strong cpCB promoter, even though the CryIVD gene contains 19
 CC AUA which are generally poorly translated (if at all) in
 CC cyanobacteria.
 SQ Sequence 643 AA;

Query Match 42.2%; Score 65; DB 18; Length 643;
 Best Local Similarity 50.0%; Pred. No. 3.98e+01;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 544 yklirrvpyrpl 557
 |::|:|:|:|
 QY 1 YRLAIRLNERVLA 14

RESULT 13
 ID P91462 standard; protein; 643 AA.
 AC P91462;
 DT 09-JAN-1990 (first entry).
 DE 67-kD protein toxin.
 KW cryd ; Bacillus thuringiensis; biopesticide.
 OS Bacillus thuringiensis var. israelensis.
 PN W08907605-A.
 PD 24-AUG-1989.
 PF 17-FEB-1989; U00663.
 PR 19-FEB-1988; US-158176.
 PA (ECOG) Ecogen Inc.
 PI Donovan WP.
 DR WPI: 89-263682/36.
 DR N-PSDB; N90712.
 DT Bacillus thuringiensis var israelensis cry D toxin gene and proteins
 PT - used for producing insecticide compsns. active against Dipteran species
 PS claim 2; fig 2; 58pp; English.
 CC The 67kD protein encoded by the gene has insecticidal activity against
 CC dipteran larvae.
 SQ Sequence 643 AA;

Query Match 42.2%; Score 65; DB 1; Length 643;
 Best Local Similarity 50.0%; Pred. No. 3.98e+01;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 544 ykllirvrvpyrlp 557
 :| | | | |
 QY 1 YRLAIRLNERVRLA 14

RESULT 14
 ID R20796 standard; Protein; 485 AA.

AC R20796;
 DT 19-MAY-1992 (first entry)
 DE EHV-4 GC.
 KW Equine herpes virus-4; glycoprotein gC; antigenic; vaccine;
 KW alphaherpesvirus; respiratory disease; cellular attachment;
 KW pathogenic.

OS Equine herpesvirus-4.
 FH Key Location/Qualifiers
 FT Peptide 1..32
 FT /label= signal_peptide
 FT Protein 33..485
 FT /label= EHV-4_gC
 FT Domain 33..444
 FT /note= "external domain contg. 11 N-linked
 FT glycosylation sites."
 FT Domain 445..468
 FT /note= "transmembrane domain"
 FT Domain 469..485
 FT /note= "hydrophilic cytoplasmic domain"
 FT Misc-difference 409
 FT /note= "antigenic site"
 PN W09201057-A.

PD 23-JAN-1992.
 PR 04-JUL-1991; G01091.
 PR 06-JUL-1990; GB-014950.
 PA (UNIU) UNIV OF GLASGOW.
 PA (EQUI-) EQUINE VIROLOGY RES FOUN.
 PI Nicolson L, Onions DE;
 DR WPI; 92-056872/07.
 DR N-PSDB; Q20995.
 PT Nucleic acid sequence encoding EHV-4 gH or gC protein - used to
 PT produce a vaccine for protection of horses against EHV-4
 PT infection
 PS Claim 7; Page 23; 29pp; English.

CC The sequence (SEQ ID no 2) was deduced from the nucleic acid
 CC sequence obtd. by screening a BamHI library constructed from EHV-4
 CC infected equine dermal cells (NBL-6). The gC protein is homologous
 CC to its gC counterpart of other herpesviruses and is characterised
 CC by conserved regions within the gC homologues (see feature table).
 CC gC homologues comprise inter alia conserved amino acids in the
 CC C-terminal half positioned around six sites of cysteine conservation
 CC at residues 256, 318, 357, 361, 390 and 416, in this sequence, implying
 CC some degree of conservation of secondary and tertiary structure
 CC between gC homologues, presumably involving disulphide bonding.
 CC EHV-4 gC has at Asp 409 a site capable of eliciting an immune
 CC response. Vaccines derived from this sequence can be prepd., and
 CC they may be used to protect horses against EHV-4 infection,
 CC inducing a higher level of immunity and less side-effects than
 CC other live virus vaccines.
 CC See also R20795.
 SQ Sequence 485 AA;

Query Match 40.9%; Score 63; DB 4; Length 485;
 Best Local Similarity 70.0%; Pred. No. 5.73e+01;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 120 yrleihngr 129
 :| | | | |
 QY 1 YRLAIRLNER 10

RESULT 15
 ID R30168 standard; Protein; 597 AA.

AC R30168;
 DT 18-MAY-1993 (first entry)
 DE Novel intestinal oncofetal gene product.

KW oncofoetal; onco-foetal; onco-fetal; intestine; gastrointestinal;
 KW cancer; tumour; growth; benign; malignant; neoplasm; metastasis.
 OS Homo sapiens.
 PN US5171850-A.
 PD 15-DEC-1992.
 PF 31-AUG-1988; 239084.
 PR 31-AUG-1988; US-239084.
 PA (ONTA-) ONTARIO CANCER INST.
 PI Buick RN, Filmus JE;
 DR WPI; 93-008640/01.
 DR N-PSDB; Q33008.

PT DNA or RNA molecule encoding intestinal onco-foetal gene - useful
 PT for detecting neoplastic cells, esp. intestinally-originating
 PT prim. and metastatic tumours
 PS Claim 1; Fig 8; 12pp; English.
 CC This sequence represents the novel intestinal oncofoetal gene
 CC product. It can be used to produce antibodies for detecting the
 CC intestinal oncofetal gene product. The encoding DNA and RNA can be
 CC used as probes for screening samples for the intestinal oncofetal
 CC gene or gene transcripts for detection of neoplastic cells, esp.
 CC intestinally-originating primary and metastatic tumours.
 SQ Sequence 597 AA;

Query Match 40.9%; Score 63; DB 6; Length 597;
 Best Local Similarity 46.2%; Pred. No. 5.73e+01;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 75 kmeekyqltarln 87
 :| | | | |
 QY 6 RLNERYRLAIRLN 18

Search completed: Thu May 22 08:35:34 1997
 Job time : 13 secs.

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.

Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.

Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:32:44 1997; MasPar time 2.31 Seconds

Tabular output not generated.
183.472 Million cell updates/sec

Title: >US-08-653-294-26
Description: (1-20) from US08653294.pep
Perfect Score: 154
Sequence: 1 YRLAIRLNERENLRALRY 20

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 31.472; Variance 50.872; scale 0.619

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------------|------------------------|-----------|
| 1 | 77 | 50.0 | 359 | 1 B01_PANTR | CHLA CLASS I HISTOCOMP | 7.49e-02 |
| 2 | 77 | 50.0 | 362 | 5 HLAH_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 3 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 4 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 5 | 77 | 50.0 | 362 | 1 B01_GORGO | CLASS I HISTOCOMPATIB | 7.49e-02 |
| 6 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 7 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 8 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 9 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 10 | 77 | 50.0 | 362 | 1 B01_GORGO | CLASS I HISTOCOMPATIB | 7.49e-02 |
| 11 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 12 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 13 | 77 | 50.0 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 14 | 77 | 50.0 | 362 | 1 B01_GORGO | CLASS I HISTOCOMPATIB | 7.49e-02 |
| 15 | 77 | 50.0 | 365 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 16 | 77 | 50.0 | 365 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 7.49e-02 |
| 17 | 77 | 47.4 | 365 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 3.43e-01 |
| 18 | 73 | 47.4 | 365 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 3.43e-01 |
| 19 | 70 | 45.5 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 1.04e+00 |
| 20 | 70 | 45.5 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 1.04e+00 |
| 21 | 70 | 45.5 | 362 | 1 B01_HUMAN | HLA CLASS I HISTOCOMP | 1.04e+00 |
| 22 | 70 | 45.5 | 3712 | 1 ACV5_CEPAC | DELTA-(L-ALPHA-AMINO | 1.04e+00 |

| | | | | | | |
|----|----|------|-----|---------------|-----------------------|----------|
| 23 | 69 | 44.8 | 388 | 7 PAM_STRPV | PLASMINOGEN-BINDING P | 1.49e+00 |
| 24 | 67 | 43.5 | 380 | 10 VINT_BPP21 | INTEGRASE | 3.05e+00 |
| 25 | 66 | 42.9 | 847 | 8 RELA_STRCO | GTP PYROPHOSPHOKINASE | 4.33e+00 |
| 26 | 66 | 42.9 | 882 | 3 ENV_SIVML | ENVELOPE POLYPROTEIN | 6.13e+00 |
| 27 | 65 | 42.2 | 798 | 5 ITB7_HUMAN | INTEGRIN BETA-7 SUBUN | 6.13e+00 |
| 28 | 65 | 42.2 | 806 | 5 ITB7_MOUSE | INTEGRIN BETA-7 SUBUN | 6.13e+00 |
| 29 | 65 | 42.2 | 852 | 2 CLPB_CORGL | CLPB PROTEIN | 6.13e+00 |
| 30 | 64 | 41.6 | 337 | 3 DFRA_VITV1 | DIHYDROFLAVONOL-4-RED | 8.65e+00 |
| 31 | 64 | 41.6 | 365 | 1 LA04_GORGO | CLASS I HISTOCOMPATIB | 8.65e+00 |
| 32 | 64 | 41.6 | 517 | 6 NCAP_SENDZ | NUCLEOCAPSID PROTEIN | 8.65e+00 |
| 33 | 64 | 41.6 | 880 | 3 ENV_SIVML | ENVELOPE POLYPROTEIN | 8.65e+00 |
| 34 | 64 | 41.6 | 881 | 3 ENV_SIVMK | ENVELOPE POLYPROTEIN | 8.65e+00 |
| 35 | 63 | 40.9 | 250 | 10 UNG_HCMVA | URACIL-DNA GLYCOSYLAS | 1.21e+01 |
| 36 | 63 | 40.9 | 351 | 2 CBIG_SALTY | CBIG PROTEIN | 1.21e+01 |
| 37 | 63 | 40.9 | 433 | 4 HEM2_SPIOL | DELTA-AMINOLEVULINIC | 1.21e+01 |
| 38 | 63 | 40.9 | 443 | 11 YV16_MYCLE | PROBABLE SENSOR-LIKE | 1.21e+01 |
| 39 | 63 | 40.9 | 485 | 10 VGLC_HSVF4 | GLYCOPROTEIN C PRECUR | 1.21e+01 |
| 40 | 63 | 40.9 | 517 | 6 NCAP_SENDE | NUCLEOCAPSID PROTEIN | 1.21e+01 |
| 41 | 63 | 40.9 | 711 | 5 HGFL_HUMAN | HEPATOCYTE GROWTH FAC | 1.21e+01 |
| 42 | 62 | 40.3 | 370 | 5 HUPK_RHILV | HUPK PROTEIN | 1.70e+01 |
| 43 | 62 | 40.3 | 380 | 11 YXEP_BACSU | HYPOTHEICAL 41.6 KD | 1.70e+01 |
| 44 | 62 | 40.3 | 524 | 6 NCAP_SENDS | NUCLEOCAPSID PROTEIN | 1.70e+01 |
| 45 | 62 | 40.3 | 661 | 8 RDGC_DRONE | SERINE/THREONINE PROT | 1.70e+01 |

ALIGNMENTS

RESULT 1
ID 1B01_PANTR STANDARD; PRT; 359 AA.

AC P13750;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR (FRAGMENT).
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; PRIMATES.
RP [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 89030641.
RA MAYER W.B., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G., KLEIN J.,
RA KLEIN J.,
RL EMBO J. 7:2765-2774(1988).
RN [2]
RP REVISIONS.
RA MAYER W.B.;
RL SUBMITTED (FEB-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
CC EMBL; X13115; G755776; -.
DR PIR; S03537; S03537.
DR HSP; P03989; IHS4.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 20
FT CHAIN 21 359
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN.
FT DOMAIN 21 110
FT DOMAIN 111 202
FT DOMAIN 203 294
FT DOMAIN 295 305
FT TRANSMEM 306 329
FT DOMAIN 330 359
FT DISULFID 121 184
FT DISULFID 223 279
FT CARBOHYD 106 106
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 359 AA; 40173 MW; 5395FFC9 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 359;

```

Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 rentrialry 104
QY 11 RENLRIALRY 20

RESULT 2
ID HLA_HUMAN STANDARD; PRT; 362 AA.
AC P01893;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
DE (HLA-AR) (HLA-12.4).
GN HLAH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82151002.
RA MALISSEN M., MALISSEN B., JORDAN B.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; V00526; G386873; ALT_INIT.
DR PIR; A02189; HLH12.
DR HSSP; P03989; 1HSA.
DR MIM; 142925; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40850 MW; 5610F63 CRC32;

Query Match 50.0%; Score 77; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
QY 11 RENLRIALRY 20

RESULT 3
ID LB47_HUMAN STANDARD; PRT; 362 AA.
AC P30487;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89235215.
RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;

Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
QY 11 RENLRIALRY 20

RESULT 4
ID LB53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M22799; G553538; ALT SEQ.
DR EMBL; M22793; G553538; JOINED.
DR EMBL; M22794; G553538; JOINED.
DR EMBL; M22795; G553538; JOINED.
DR EMBL; M22796; G553538; JOINED.
DR EMBL; M22797; G553538; JOINED.
DR EMBL; M22798; G553538; JOINED.
DR PIR; B30345; B30345.
DR PIR; B30548; B30548.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.

```

```

J. IMMUNOL. 142:3937-3950(1989).
[2]
RN REVISIONS TO 78.
RX MEDLINE: 93056529.
RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
RA WILLIAMS R.C., PARHAM P.;
RL J. IMMUNOL. 149:3563-3568(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M24037; G407191; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
QY 11 RENLRIALRY 20

RESULT 4
ID LB53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M22799; G553538; ALT SEQ.
DR EMBL; M22793; G553538; JOINED.
DR EMBL; M22794; G553538; JOINED.
DR EMBL; M22795; G553538; JOINED.
DR EMBL; M22796; G553538; JOINED.
DR EMBL; M22797; G553538; JOINED.
DR EMBL; M22798; G553538; JOINED.
DR PIR; B30345; B30345.
DR PIR; B30548; B30548.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.

```

```

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 ALPHA CHAIN BW-52(B-5) B*5201.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT CARBOHYD 110 110 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40521 MW; 3B436FEB CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 RENLIRIALRY 20

RESULT 5
ID 1B01_GORGO STANDARD; PRT: 362 AA.
AC P30379;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; X60255; G228666; -.
DR PIR; JH0539; JH0539.
DR HSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT DISULFID 125 188 CYTOPLASMIC TAIL.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 RENLIRIALRY 20

RESULT 6
ID 1B54_HUMAN STANDARD; PRT: 362 AA.
AC P30379;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; X60255; G228666; -.
DR PIR; JH0539; JH0539.
DR HSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT DISULFID 125 188 CYTOPLASMIC TAIL.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 RENLIRIALRY 20

RESULT 7
ID 1B60_HUMAN STANDARD; PRT: 362 AA.
AC P18465;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.
RA ENNIS P.D.; ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.

```

```

AC P30491;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
PRECURSOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91033941.
RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,
RA TAKIGUCHI M.,
RL IMMUNOGENETICS 32:195-199(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M58636; G187757; -.
DR PIR; A45834; A45834.
DR HSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 ALPHA CHAIN BW-53 B*5301.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 RENLIRIALRY 20

RESULT 7
ID 1B60_HUMAN STANDARD; PRT: 362 AA.
AC P18465;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.
RA ENNIS P.D.; ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.

```

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

DR EMBL; M32318; G307222; -.

DR EMBL; X55711; G32181; -.

DR PIR; S12622; S12622.

DR PIR; D35997; D35997.

DR HSSP; P03989; 1HSA.

DR MIM; 142830; -.

DR PROSITE; PS00290; IG_MHC.

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

FT SIGNAL 1 24

FT CHAIN 25 362

FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN B-57(B-17) B*5701.

FT DOMAIN 25 114

FT EXTRACELLULAR ALPHA-1.

FT DOMAIN 115 206

FT EXTRACELLULAR ALPHA-2.

FT DOMAIN 207 298

FT EXTRACELLULAR ALPHA-3.

FT DOMAIN 299 308

FT CONNECTING PEPTIDE.

FT TRANSMEM 309 332

FT CYTOPLASMIC TAIL.

FT CARBOHYD 110 110

FT BY SIMILARITY.

FT DISULFID 125 188

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT CHAIN 25 362

FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN B-27 B*2702.

FT DOMAIN 25 114

FT EXTRACELLULAR ALPHA-1.

FT DOMAIN 115 206

FT EXTRACELLULAR ALPHA-2.

FT DOMAIN 207 298

FT EXTRACELLULAR ALPHA-3.

FT DOMAIN 299 308

FT CONNECTING PEPTIDE.

FT TRANSMEM 309 332

FT CYTOPLASMIC TAIL.

FT CARBOHYD 110 110

FT BY SIMILARITY.

FT DISULFID 125 188

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).

DR EMBL; M32318; G307222; -.

DR EMBL; X55711; G32181; -.

DR PIR; S12622; S12622.

DR PIR; D35997; D35997.

DR HSSP; P03989; 1HSA.

DR MIM; 142830; -.

DR PROSITE; PS00290; IG_MHC.

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

FT SIGNAL 1 24

FT CHAIN 25 362

FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN B-57(B-17) B*5701.

FT DOMAIN 25 114

FT EXTRACELLULAR ALPHA-1.

FT DOMAIN 115 206

FT EXTRACELLULAR ALPHA-2.

FT DOMAIN 207 298

FT EXTRACELLULAR ALPHA-3.

FT DOMAIN 299 308

FT CONNECTING PEPTIDE.

FT TRANSMEM 309 332

FT CYTOPLASMIC TAIL.

FT CARBOHYD 110 110

FT BY SIMILARITY.

FT DISULFID 125 188

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

FT DISULFID 227 283

FT BY SIMILARITY.

```

ID 1B03_GORGO STANDARD; PRT; 362 AA.
AC P30381;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078660.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X60254; G22870; -.
DR PIR; JH0541; JH0541.
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 238
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 362 AA; 40248 MW; FEA6A941 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 renltrialry 20

RESULT 11
ID 1B49_HUMAN STANDARD; PRT; 362 AA.
AC P18464;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*5101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89233295.
RA POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;

```

```

RL IMMUNOGENETICS 29:297-307(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M32319; G307223; -.
DR EMBL; M22792; G553533; ALT_SEQ.
DR EMBL; M22786; G553533; JOINED.
DR EMBL; M22787; G553533; JOINED.
DR EMBL; M22788; G553533; JOINED.
DR EMBL; M22789; G553533; JOINED.
DR EMBL; M22790; G553533; JOINED.
DR EMBL; M22791; G553533; JOINED.
DR EMBL; L41087; G735902; -.
DR PIR; A30345; A30345.
DR PIR; A30548; A30548.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 renltrialry 20

RESULT 12
ID 1B61_HUMAN STANDARD; PRT; 362 AA.
AC P30497;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*5702 ALPHA CHAIN
DE PRECURSOR (BW57.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X61707; G32187; -.
DR PIR; S16774; S16774.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

```

FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN B-57(B-17) B*5702.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40342 MW; 628C2156 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
 |||||
 QY 11 RENRIALRY 20

RESULT 13
 ID 1B52_HUMAN STANDARD; PRT; 362 AA.
 AC P30489;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
 DE PRECURSOR.
 GN HLAB.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92269955.
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
 RL NATURE 357:326-329(1992).
 CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC EMBL; Z15143; G28235; -.
 DR HSSP; P03989; ILSA.
 DR MIM; 142830; -.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN B-51(B-5) B*5104.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
 |||||
 QY 11 RENRIALRY 20

RESULT 14
 ID 1B02_GORGO STANDARD; PRT; 362 AA.
 AC P30380;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
 DE GORILLA GORILLA (LOWLAND GORILLA).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92078860.
 RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
 RL J. EXP. MED. 174:1491-1509(1991).
 CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC EMBL; X60693; G22868; -.
 DR FIR; JH0540; JH0540.
 DR HSSP; P03989; ILSA.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT GOGO-B0102 ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40204 MW; 3CF119AD CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
 |||||
 QY 11 RENRIALRY 20

RESULT 15
 ID 1A23_HUMAN STANDARD; PRT; 365 AA.
 AC P30447;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
 DE PRECURSOR.
 GN HLA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A. (A*2301).
 RX MEDLINE; 92104637.
 RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;
 RL IMMUNOGENETICS 35:41-45(1992).
 CC -|- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -|- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC -|- POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A*2301 WHICH IS
 SHOWN HERE.
 CC EMBL; M64742; G187618; -.
 DR HSSP; P01892; 1HGG.
 DR MIM; 142800; -.

```

DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN A-23(A9);
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 365 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 365 AA; 40732 MW; BIC21094 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
Oy 11 RENLRYALRY 20

```

Search completed: Thu May 22 08:32:51 1997
Job time : 7 secs.

THIS PAGE BLANK (USPTO)

WIREH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:33:09 1997; MasPar time 3.22 Seconds
Tabular output not generated. 176.841 Million cell updates/sec

Title: >US-08-653-294-26
Description: (1-20) from US08653294.pep
Perfect Score: 154
Sequence: 1 YRLAIRLNERENLRALRY 20

Scoring table:
PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 30.116; Variance 61.232; scale 0.492

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description | Pred. No. |
|------------|-------|---------------|--------|----|------------------------------|-----------|
| 1 | 77 | 50.0 | 273 | 13 | I38509 MHC class I histocomp | 5.91e-01 |
| 2 | 77 | 50.0 | 274 | 13 | I54463 MHC HLA-B*38 chain - | 5.91e-01 |
| 3 | 77 | 50.0 | 354 | 13 | I59308 class I histocompati | 5.91e-01 |
| 4 | 77 | 50.0 | 354 | 13 | I80168 class I histocompati | 5.91e-01 |
| 5 | 77 | 50.0 | 354 | 13 | I80167 class I histocompati | 5.91e-01 |
| 6 | 77 | 50.0 | 355 | 13 | I80171 class I histocompati | 5.91e-01 |
| 7 | 77 | 50.0 | 355 | 13 | I80169 class I histocompati | 5.91e-01 |
| 8 | 77 | 50.0 | 359 | 2 | HLHU12 MHC class I histocom | 5.91e-01 |
| 9 | 77 | 50.0 | 362 | 6 | JH0539 MHC class I histocom | 5.91e-01 |
| 10 | 77 | 50.0 | 362 | 6 | B30345 MHC class I histocom | 5.91e-01 |
| 11 | 77 | 50.0 | 362 | 13 | I84486 transmembrane glycop | 5.91e-01 |
| 12 | 77 | 50.0 | 362 | 6 | JH0540 class I histocompati | 5.91e-01 |
| 13 | 77 | 50.0 | 362 | 6 | S24434 class I histocompati | 5.91e-01 |
| 14 | 77 | 50.0 | 362 | 6 | A30345 MHC class I histocom | 5.91e-01 |
| 15 | 77 | 50.0 | 362 | 13 | I37521 HLA-B*57.2 antigen - | 5.91e-01 |
| 16 | 77 | 50.0 | 362 | 13 | I59633 MHC HLA-B transmembr | 5.91e-01 |
| 17 | 77 | 50.0 | 362 | 6 | JH0541 class I histocompati | 5.91e-01 |
| 18 | 77 | 50.0 | 362 | 13 | I84490 lymphocyte antigen - | 5.91e-01 |
| 19 | 77 | 50.0 | 362 | 13 | I62045 gene HLA B-1517 prot | 5.91e-01 |
| 20 | 77 | 50.0 | 362 | 6 | A45834 MHC class I histocom | 5.91e-01 |
| 21 | 77 | 50.0 | 362 | 2 | HLHUB8 MHC class I histocom | 5.91e-01 |

| | | | | | | |
|----|----|------|------|----|------------------------------|----------|
| 22 | 77 | 50.0 | 362 | 13 | I37120 MHC class I HLA-B*51 | 5.91e-01 |
| 23 | 77 | 50.0 | 363 | 16 | S07113 class I histocompati | 5.91e-01 |
| 24 | 77 | 50.0 | 363 | 13 | I36957 MHC ChLA chain - chi | 5.91e-01 |
| 25 | 77 | 50.0 | 363 | 6 | S03537 class I histocompati | 5.91e-01 |
| 26 | 77 | 50.0 | 364 | 6 | D35997 MHC class I histocom | 5.91e-01 |
| 27 | 77 | 50.0 | 365 | 13 | I54493 HLA-A protein - huma | 5.91e-01 |
| 28 | 77 | 50.0 | 365 | 13 | I54416 HLA-AW24 protein - h | 5.91e-01 |
| 29 | 73 | 47.4 | 274 | 2 | HLHU32 MHC class I histocom | 2.08e+00 |
| 30 | 73 | 47.4 | 364 | 6 | A35997 MHC class I histocom | 2.08e+00 |
| 31 | 70 | 45.5 | 362 | 6 | A45850 MHC class I histocom | 5.22e+00 |
| 32 | 70 | 45.5 | 362 | 6 | S25415 class I histocompati | 5.22e+00 |
| 33 | 70 | 45.5 | 362 | 13 | I61861 MHC HLA-B44.2 chain | 5.22e+00 |
| 34 | 70 | 45.5 | 362 | 13 | I54442 MHC HLA-B13 precursor | 5.22e+00 |
| 35 | 70 | 45.5 | 3712 | 2 | YGCEVC alpha-aminoadipyl-cy | 5.22e+00 |
| 36 | 69 | 44.8 | 388 | 7 | A49545 plasminogen-binding | 7.06e+00 |
| 37 | 66 | 42.9 | 88 | 16 | S60814 M protein precursor | 1.72e+01 |
| 38 | 66 | 42.9 | 408 | 7 | S30283 protein M precursor | 1.72e+01 |
| 39 | 66 | 42.9 | 436 | 7 | S30284 M protein precursor | 1.72e+01 |
| 40 | 66 | 42.9 | 881 | 4 | VCLJG3 env polyprotein - si | 1.72e+01 |
| 41 | 65 | 42.2 | 763 | 11 | S17998 gene COX1 intron 4 p | 2.30e+01 |
| 42 | 65 | 42.2 | 798 | 7 | A40526 integrin beta-7 chai | 2.30e+01 |
| 43 | 65 | 42.2 | 806 | 7 | A46271 integrin beta-7 chai | 2.30e+01 |
| 44 | 65 | 42.2 | 869 | 8 | A47665 env protein gp120(cl | 2.30e+01 |
| 45 | 64 | 41.6 | 881 | 8 | S03068 env protein - human | 3.06e+01 |

ALIGNMENTS

RESULT 1
ENTRY I38509 #type fragment
TITLE MHC class I histocompatibility antigen - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 06-Sep-1996
ACCESSIONS I38509
REFERENCE I38509
#authors Cerb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
#journal Tissue Antigens (1994) 44:271-273
#title HLA-B*5105 a newly identified B51 IEF variant.
#cross-references MUID:95176331
#accession I38509
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-273 ##label RES
#cross-references EMBL:U06697; NID:g469544; CDS_PID:g469545
GENETICS
#note gene name HLA-B
SUMMARY #length 273 #checksum 6533

Query Match 50.0%; Score 77; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 renirialry 83
|||||||
Qy 11 RENIRIALRY 20

RESULT 2
ENTRY I54463 #type fragment
TITLE MHC HLA-B*38 chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 07-Jun-1996
ACCESSIONS I54463
REFERENCE I54463

#authors Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.;
Weiss, E.; Schmidt, H.
#journal Immunogenetics (1989) 30:200-207
#title Genetic and serological heterogeneity of the supertypic HLA-B
locus specificities Bw4 and Bw6.
#cross-references MUID:89379286
#accession I54463

```
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues    1-274 ##label RES
##cross-references GB:M29864; NID:g187674; CDS_PID:g187675
SUMMARY      #length 274 #checksum 1031
```

```
Query Match      50.0%; Score 77; DB 13; Length 274;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 75 renltrialy 84
|||||
QY 11 RENLRIALRY 20
```

```
RESULT 3          #type fragment
ENTRY      class I histocompatibility antigen - pygmy chimpanzee
TITLE      (fragment)
ORGANISM    #formal_name Pan paniscus #common_name pygmy chimpanzee,
            bonobo
DATE        31-May-1996 #sequence_revision 31-May-1996 #text_change
            31-May-1996
ACCESSIONS  I59308
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I59308
##status    preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues  1-354 ##label RES
##cross-references EMBL:U05575; NID:g454767; CDS_PID:g454768
SUMMARY      #length 354 #checksum 3211
```

```
Query Match      50.0%; Score 77; DB 13; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20
```

```
RESULT 4          #type fragment
ENTRY      class I histocompatibility antigen - chimpanzee (fragment)
TITLE      #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM    24-May-1996 #sequence_revision 24-May-1996 #text_change
DATE        24-May-1996
ACCESSIONS  I80168
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80168
##status    preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues  1-354 ##label RES
##cross-references EMBL:U05579; NID:g454775; CDS_PID:g454776
SUMMARY      #length 354 #checksum 5067
```

```
Query Match      50.0%; Score 77; DB 13; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20
```

```
RESULT 4          #type fragment
ENTRY      class I histocompatibility antigen - chimpanzee (fragment)
TITLE      #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM    24-May-1996 #sequence_revision 24-May-1996 #text_change
DATE        24-May-1996
ACCESSIONS  I80168
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80168
##status    preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues  1-354 ##label RES
##cross-references EMBL:U05579; NID:g454775; CDS_PID:g454776
SUMMARY      #length 354 #checksum 5067
```

```
Query Match      50.0%; Score 77; DB 13; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20
```

```
RESULT 7          #type fragment
ENTRY      class I histocompatibility antigen - chimpanzee (fragment)
TITLE      #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM    24-May-1996 #sequence_revision 24-May-1996 #text_change
DATE        24-May-1996
ACCESSIONS  I80169
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80168
##status    preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues  1-354 ##label RES
##cross-references EMBL:U05579; NID:g454775; CDS_PID:g454776
SUMMARY      #length 354 #checksum 5067
```

```
Query Match      50.0%; Score 77; DB 13; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20
```

```
RESULT 5          #type fragment
ENTRY      class I histocompatibility antigen - pygmy chimpanzee
TITLE      (fragment)
ORGANISM    #formal_name Pan paniscus #common_name pygmy chimpanzee,
            bonobo
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
            24-May-1996
ACCESSIONS  I80167
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80167
##status    preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues  1-354 ##label RES
##cross-references EMBL:U05578; NID:g454773; CDS_PID:g454774
SUMMARY      #length 354 #checksum 3983
```

```
Query Match      50.0%; Score 77; DB 13; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20
```

```
RESULT 6          #type fragment
ENTRY      class I histocompatibility antigen - chimpanzee (fragment)
TITLE      #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM    24-May-1996 #sequence_revision 24-May-1996 #text_change
DATE        24-May-1996
ACCESSIONS  I80171
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80171
##status    preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues  1-355 ##label RES
##cross-references EMBL:U05582; NID:g454781; CDS_PID:g454782
SUMMARY      #length 355 #checksum 6021
```

```
Query Match      50.0%; Score 77; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20
```

```
RESULT 7          #type fragment
ENTRY      class I histocompatibility antigen - chimpanzee (fragment)
TITLE      #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM    24-May-1996 #sequence_revision 24-May-1996 #text_change
DATE        24-May-1996
ACCESSIONS  I80169
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80171
##status    preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues  1-355 ##label RES
##cross-references EMBL:U05582; NID:g454781; CDS_PID:g454782
SUMMARY      #length 355 #checksum 6021
```

```
Query Match      50.0%; Score 77; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20
```

```
RESULT 7          #type fragment
ENTRY      class I histocompatibility antigen - chimpanzee (fragment)
TITLE      #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM    24-May-1996 #sequence_revision 24-May-1996 #text_change
DATE        24-May-1996
ACCESSIONS  I80169
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
```

```

#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80169
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues_type 1-355 ##label RES
#cross-references EMBL:U05580; NID:g454777; CDS_PID:g454778
SUMMARY    #length 355 #checksum 4603

Query Match      50.0%; Score 77; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 5,91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 renrtrialry 100
|||||
Qy 11 RENLRIALRY 20

RESULT 8
ENTRY HLH012 #type complete
TITLE MHC class I histocompatibility antigen HLA alpha chain
ORGANISM precursor (clone pHLA 12.4) - human
#formal_name Homo sapiens #common_name man
DATE 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change
15-Jun-1996
ACCESSIONS A02189
REFERENCE Malissen, M.; Malissen, B.; Jordan, B.R.
#authors Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
#journal Exon/intron organization and complete nucleotide sequence of
#title an HLA gene.
#cross-references MUID:82151002
#accession A02189
#molecule_type DNA
#residues_type 1-359 ##label MAL
COMMENT The seven exons correspond approximately to the domain structure of
this chain.
GENETICS
#map_position 6p21.3
#introns 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
FEATURE
1-21 #domain signal sequence #status predicted #label SIG\
22-359 #product class I histocompatibility antigen HLA alpha
chain #status predicted #label MAT\
22-304 #domain extracellular #status predicted #label EX1\
22-111 #domain alpha-1 #label EX1\
112-203 #domain alpha-2 #label EX2\
217-282 #domain immunoglobulin homology #label IMM\
305-329 #domain transmembrane #status predicted #label TMM\
335-359 #domain intracellular #status predicted #label INN\
107 #binding_site carbohydrate (Asn) (covalent) #status
predicted\
224-280 #disulfide_bonds #status predicted
SUMMARY #length 359 #molecular-weight 40548 #checksum 2195

Query Match      50.0%; Score 77; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 5,91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 96 renrtrialry 105
|||||
Qy 11 RENLRIALRY 20

RESULT 9
ENTRY JH0539 #type complete
TITLE class I histocompatibility antigen Gogo-B0101 heavy chain
ORGANISM precursor - lowland gorilla
#formal_name Gorilla #common_name lowland

```

```

gorilla
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
26-Apr-1996
ACCESSIONS JH0539
REFERENCE JH0534
#authors Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
#journal J. Exp. Med. (1991) 174:1491-1509
#title Gorilla class I major histocompatibility complex alleles:
comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession JH0539
#molecule_type DNA
#residues 1-362 ##label LAW
##cross-references EMBL:X60255
##experimental_source EBV-transformed B cell
GENETICS
#introns 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
1-24 #domain signal sequence #label SIG\
25-362 #product class I histocompatibility antigen heavy chain,
Gogo-B0101 #status predicted #label CLA\
25-114 #domain alpha-1 #label AL1\
115-206 #domain alpha-2 #label AL2\
207-298 #domain alpha-3 #label AL3\
220-285 #domain immunoglobulin homology #label IMM\
299-362 #domain intracellular #label INT
SUMMARY #length 362 #molecular-weight 40170 #checksum 7327

Query Match      50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5,91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renrtrialry 108
|||||
Qy 11 RENLRIALRY 20

RESULT 10
ENTRY B30345 #type complete
TITLE MHC class I histocompatibility antigen HLA-Bw52 precursor -
human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
26-Apr-1996
ACCESSIONS B30345
REFERENCE A30345
#authors Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
P.; Kano, K.; Takiguchi, M.
#journal J. Immunol. (1989) 142:306-311
#title HLA-B51 and HLA-Bw52 differ by only two amino acids which are
in the helical region of the alpha-1 domain.
#cross-references MUID:89080265
#accession B30345
#status preliminary
#molecule_type DNA
#residues 1-362 ##label HAY
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SUMMARY #length 362 #molecular-weight 40521 #checksum 9891

Query Match      50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5,91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renrtrialry 108
|||||
Qy 11 RENLRIALRY 20

```

```

RESULT 11
ENTRY   I84486      #type complete
TITLE   Transmembrane glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I84486
REFERENCE  I38421
#authors  Hildebrand, W.H.; Domana, J.D.; Shen, S.Y.; Lau, M.;
          Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
          Bias, W.B.; Parham, P.
#journal  Tissue Antigens (1994) 43:209-218
#title    HLA-B*15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I84486
##status  preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:L15005; NID:g493154; CDS_PID:g493155
GENETICS
#note     Gene name HLA-B*1513
SUMMARY   #length 362 #molecular-weight 40378 #checksum 9463

Query Match 50.0%; Score 77; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renlrialy 108
   |||||
QY 11 RENLRIALRY 20

RESULT 12
ENTRY   JH0540      #type complete
TITLE   class I histocompatibility antigen Gogo-B0102 heavy chain
ORGANISM #formal_name Gorilla gorilla #common_name lowland
          gorilla
DATE    30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
ACCESSIONS JH0540
REFERENCE  JH0534
#authors  Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
#journal  J. Exp. Med. (1991) 174:1491-1509
#title    Gorilla class I major histocompatibility complex alleles:
          comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession JH0540
##molecule_type DNA
##residues 1-362 #label LAW
##cross-references EMBL:X60693
##experimental_source EBV-transformed B cell
GENETICS
#introns  25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE
1-24      #domain signal sequence #label SIG\
25-362    #product class I histocompatibility antigen heavy chain,
          Gogo-B0102 #status predicted #label CLA\
25-114    #domain alpha-1 #label AL1\
115-206   #domain alpha-2 #label AL2\
207-298   #domain alpha-3 #label AL3\
220-285   #domain immunoglobulin homology #label IMM\
299-362   #domain intracellular #label INT
SUMMARY   #length 362 #molecular-weight 40204 #checksum 7312

Query Match 50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renlrialy 108
   |||||
QY 11 RENLRIALRY 20

RESULT 13
ENTRY   S24434      #type complete
TITLE   class I histocompatibility antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS S24434
REFERENCE  S24027
#authors  Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
          E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
          Ghm, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal  Nature (1992) 357:329-333
#title    New recombinant HLA-B alleles in a tribe of South American
          Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession S24434
##status  preliminary
##molecule_type mRNA
##residues 1-362 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
220-285   #domain immunoglobulin homology #label IMM
SUMMARY   #length 362 #molecular-weight 40462 #checksum 9855

Query Match 50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renlrialy 108
   |||||
QY 11 RENLRIALRY 20

RESULT 14
ENTRY   A30345      #type complete
TITLE   MHC class I histocompatibility antigen HLA-B51 precursor -
          human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
ACCESSIONS A30345; I68746
REFERENCE  A30345
#authors  Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
          P.; Kano, K.; Takiguchi, M.
#journal  J. Immunol. (1989) 142:306-311
#title    HLA-B51 and HLA-B*52 differ by only two amino acids which are
          in the helical region of the alpha-1 domain.
#cross-references MUID:89080265
#accession A30345
##status  preliminary
##molecule_type mRNA
##residues 1-362 #label HAY
REFERENCE  I54457
#authors  Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
          E.H.
#journal  Immunogenetics (1989) 29:297-307
#title    Allelic variation in HLA-B and HLA-C sequences and the
          evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68746
##status  preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-362 #label RES
##cross-references GB:L41087; NID:g735900; CDS_PID:g735902
GENETICS
#note     GDB:HLA-B
#cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology

```

```

FEATURE
220-285      #domain immunoglobulin homology #label IMM
SUMMARY      #length 362 #molecular-weight 40566 #checksum 9719

Query Match      50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renlrialy 108
|||||
QY 11 RENLRIALRY 20

RESULT 15
ENTRY      I37521      #type complete
TITLE      HLA-B*57.2 antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
          02-Jul-1996
ACCESSIONS I37521
REFERENCE   I37476
#authors   Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,
          R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
          Petzl-Erler, M.L.; Du Toit, E.D.; Parham, P.
#journal   J. Immunol. (1992) 149:3411-3415
#title     Distinctive HLA-A,B antigens of black populations formed by
          interallelic conversion.
#cross-references MUID:93056508
#accession I37521
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-362 #label RES
#cross-references EMBL:X61707; NID:g32186; CDS_PID:g32187
SUMMARY    #length 362 #molecular-weight 40342 #checksum 7369

Query Match      50.0%; Score 77; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renlrialy 108
|||||
QY 11 RENLRIALRY 20

Search completed: Thu May 22 08:33:25 1997
Job time : 16 secs.

```

THIS PAGE BLANK (USPTO)

W P S R L H
(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.

Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.

Distribution rights by Intelligenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:33:42 1997; MasPar time 2.21 Seconds
98.639 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-26
Description: (1-20) from US08653294.pep

Perfect Score: 154
Sequence: 1 YRLAIRLNRRNLRIALRY 20

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq26

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 21.097; Variance 80.944; scale 0.261

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match % | Length | ID | Description | Pred. No. |
|------------|-------|---------|--------|----|------------------------|-----------|
| 1 | 154 | 100.0 | 20 | 18 | HLA-B2702 84-75-84 pa | 1.21e-07 |
| 2 | 154 | 100.0 | 20 | 16 | HLA-B2702 CTL modul | 1.21e-07 |
| 3 | 147 | 95.5 | 20 | 16 | HLA-B2702 CTL modul | 6.09e-07 |
| 4 | 147 | 95.5 | 20 | 16 | HLA-B2702 CTL modul | 6.09e-07 |
| 5 | 140 | 90.9 | 20 | 16 | HLA-B2702 CTL modul | 3.05e-06 |
| 6 | 131 | 85.1 | 20 | 16 | HLA-B2702 CTL modul | 2.39e-05 |
| 7 | 83 | 53.9 | 20 | 16 | HLA-B2702 CTL modul | 9.02e-01 |
| 8 | 77 | 50.0 | 10 | 18 | HLA-B2702 CTL modul | 3.13e+00 |
| 9 | 77 | 50.0 | 10 | 18 | Alpha1-helix of HLA-B | 3.13e+00 |
| 10 | 77 | 50.0 | 10 | 18 | Peptide fragment of C | 3.13e+00 |
| 11 | 77 | 50.0 | 15 | 16 | HLA-B2702 CTL modul | 3.13e+00 |
| 12 | 77 | 50.0 | 25 | 18 | HLA-B2702 CTL modul | 3.13e+00 |
| 13 | 77 | 50.0 | 25 | 18 | HLA-B2702 CTL modul | 3.13e+00 |
| 14 | 77 | 50.0 | 25 | 8 | Peptide fragment of C | 3.13e+00 |
| 15 | 77 | 50.0 | 25 | 16 | HLA-B2702 CTL modul | 3.13e+00 |
| 16 | 77 | 50.0 | 25 | 8 | Peptide fragment of H | 3.13e+00 |
| 17 | 77 | 50.0 | 25 | 16 | HLA-B2702 CTL modul | 3.13e+00 |
| 18 | 77 | 50.0 | 362 | 2 | Sequence of HLA-Bw52 | 3.13e+00 |
| 19 | 77 | 50.0 | 362 | 2 | Sequence of HLA-Bw51 a | 3.13e+00 |
| 20 | 77 | 50.0 | 362 | 3 | HLA-Bw53 exon. | 3.13e+00 |

| | | | | | | | |
|----|----|------|-------|----|--------|-----------------------|----------|
| 21 | 75 | 48.7 | 10 | 16 | R83094 | HLA-B2702 CTL modul | 4.72e+00 |
| 22 | 75 | 48.7 | 10 | 18 | R95425 | HLA-B2702.75-84 (D) | 4.72e+00 |
| 23 | 70 | 45.5 | 10 | 18 | R95426 | HLA-B2702.75-84 (T) | 1.30e+01 |
| 24 | 70 | 45.5 | 10 | 16 | R83096 | HLA-B2702 CTL modul | 1.30e+01 |
| 25 | 70 | 45.5 | 10 | 16 | R83095 | HLA-B2702 CTL modul | 1.30e+01 |
| 26 | 70 | 45.5 | 20 | 16 | R95415 | HLA-B7.84-75-84 Palin | 1.30e+01 |
| 27 | 70 | 45.5 | 20 | 16 | R92913 | HLA-B7 CTL modul | 1.30e+01 |
| 28 | 70 | 45.5 | 3639 | 8 | R40227 | ACVS | 1.30e+01 |
| 29 | 70 | 45.5 | 3712 | 3 | R13896 | ACV synthetase. | 1.30e+01 |
| 30 | 65 | 42.2 | 879 | 4 | R24126 | SV4mac239 env gene pr | 3.49e+01 |
| 31 | 64 | 41.6 | 97 | 4 | R21601 | Putative transposito | 4.25e+01 |
| 32 | 64 | 41.6 | 116 | 7 | R38670 | 268-D. | 4.25e+01 |
| 33 | 63 | 40.9 | 485 | 4 | R20796 | EHV-4 9C. | 5.16e+01 |
| 34 | 63 | 40.9 | 705 | 10 | R66598 | Human L5/3 tumour sup | 5.16e+01 |
| 35 | 63 | 40.9 | 705 | 10 | R66597 | Human L5/3 tumour sup | 5.16e+01 |
| 36 | 63 | 40.9 | 711 | 10 | R66602 | Human L5/3 tumour sup | 5.16e+01 |
| 37 | 63 | 40.9 | 713 | 10 | R66603 | Encoded by full-lengt | 5.16e+01 |
| 38 | 63 | 40.9 | 15281 | 9 | R4929 | T. niveum Cyclosporin | 5.16e+01 |
| 39 | 61 | 39.6 | 10 | 8 | R41212 | Peptide fragment of C | 7.60e+01 |
| 40 | 61 | 39.6 | 10 | 18 | R95423 | HLA-B2705.75-84. | 7.60e+01 |
| 41 | 61 | 39.6 | 10 | 16 | R83075 | HLA-B2702 CTL modul | 7.60e+01 |
| 42 | 61 | 39.6 | 25 | 18 | R95417 | HLA-B2705 60-84. | 7.60e+01 |
| 43 | 61 | 39.6 | 25 | 16 | R83091 | HLA-B2702 CTL modul | 7.60e+01 |
| 44 | 61 | 39.6 | 362 | 2 | P70155 | Sequence encoded by g | 7.60e+01 |
| 45 | 61 | 39.6 | 630 | 3 | R12230 | TrpE/androgen recepto | 7.60e+01 |

ALIGNMENTS

RESULT 1
ID R95428 standard; peptide; 20 AA.
AC R95428;
DT 12-NOV-1996 (first entry)
DE HLA-B2702 84-75-84 palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW Cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C. Krensky AM;
DR WPI; 95-194027/35.
PT Compns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
SQ Sequence 20 AA;

Query Match 100.0%; Score 154; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.21e-07;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERENLRALRY 20
 |||||
 QY 1 YRLAIRLNRERENLRALRY 20

RESULT 2

ID R92907 standard; peptide; 20 AA.
 AC R92907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 154; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.21e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERENLRALRY 20
 |||||
 QY 1 YRLAIRLNRERENLRALRY 20

RESULT 3

ID R92909 standard; peptide; 20 AA.
 AC R92909;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 95.5%; Score 147; DB 16; Length 20;

Best Local Similarity 95.0%; Pred. No. 6.09e-07;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERENLRALRY 20
 |||||
 QY 1 YRLAIRLNRERENLRALRY 20

RESULT 4

ID R92908 standard; peptide; 20 AA.
 AC R92908;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 95.5%; Score 147; DB 16; Length 20;

Best Local Similarity 95.0%; Pred. No. 6.09e-07;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERENLRALRY 20
 |||||
 QY 1 YRLAIRLNRERENLRALRY 20

RESULT 5

ID R92910 standard; peptide; 20 AA.
 AC R92910;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.

(STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;
 SQ
 Query Match 90.9%; Score 140; DB 16; Length 20;
 Best Local Similarity 90.0%; Pred. No. 3.05e-06;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 1 yrlairlnrrenrltrialy 20
 QY 1 YRLAIRLNRRERENRLIALRY 20
 RESULT 6
 ID R95430 standard; peptide; 20 AA.
 AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-757/75-84 palindromic.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; PS-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B2702 60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.
 CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 CC Sequence 20 AA;
 SQ
 Query Match 85.1%; Score 131; DB 18; Length 20;
 Best Local Similarity 94.7%; Pred. No. 2.39e-05;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 yrlairlnrrenrltrialr 19
 QY 1 YRLAIRLNRRERENRLIALR 19
 RESULT 7
 ID R92911 standard; peptide; 20 AA.
 AC R92911;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;
 SQ
 Query Match 53.9%; Score 83; DB 16; Length 20;
 Best Local Similarity 65.0%; Pred. No. 9.02e-01;
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 DB 1 yrlairlnrrenrltrialr 20
 QY 1 YRLAIRLNRRERENRLIALR 19
 RESULT 8
 ID R83062 standard; peptide; 10 AA.
 AC R83062;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Claim 15; Page 9; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialry 10
 QY 11 RENLRIALRY 20

RESULT 9

ID R95413 standard; peptide; 10 AA.
 AC R95413; 12-NOV-1996 (first entry)
 DE Alpha-helix of HLA-B2702.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW Cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.

PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC This sequence represents the alpha-helix of the
 CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702-60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialry 10
 QY 11 RENLRIALRY 20

RESULT 10

ID R41208 standard; peptide; 10 AA.
 AC R41208;
 DR 15-MAR-1994 (first entry)

DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW Parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN WO9317699-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI; 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 11; Page 54; 61pp; English.
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
 CC activity, either by inhibition or stimulation. It can be used
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 CC This peptide sequence is more commonly found within larger peptide
 CC compounds of not more than 30 amino acids in length.
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialry 10
 QY 11 RENLRIALRY 20

RESULT 11

ID R92912 standard; peptide; 15 AA.
 AC R92912;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.70-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 15 AA;

Query Match 50.0%; Score 77; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 renltrialry 15
 QY 11 RENLRIALRY 20

CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents
 CC HLA-B2702.60-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC this sequence, induces calcium influx, and inhibits cytotoxic T
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can
 CC be screened for their effect on the cytolytic activity of T-cells, by
 CC combining them with the extracellular portion of p74 and determining the
 CC amount of binding between the candidate compound and p74. Modulation of
 CC CTL activity can be inhibited in a cellular composition containing
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the
 CC extracellular portion of p74, in an amount sufficient to compete with p74
 CC for the binding of the p74 ligand.
 CC Sequence 25 AA;

Query Match 50.0%; Score 77; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renltrialy 25
 |||||
 QY 11 RENLRIALRY 20

RESULT 14

ID R41205 standard; peptide; 25 AA.
 AC R41205;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN W09317699-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 8; Page 53; 61pp; English.
 CC The peptide (or a fragment of at least 10 amino acids, joined at at
 CC least one terminus to a sequence other than that of wild type HLA
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
 CC either by inhibition or stimulation. It can be used for
 CC inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 CC Sequence 25 AA;

Query Match 50.0%; Score 77; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renltrialy 25
 |||||
 QY 11 RENLRIALRY 20

RESULT 15

ID R83093 standard; peptide; 25 AA.
 AC R83093;
 DT 16-MAY-1996 (first entry)
 DE HLAB38 CTL modulating peptide (B38.6084).

CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC a T-cell lysate. p74 is a T-cell surface membrane protein associated
 CC with T-cell activation in mammalian T-cells, and is also immunologically
 CC cross reactive with the heat shock protein Hsc70. p74 is found in a
 CC limited number of cell types, but is particularly expressed on B and T
 CC cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 CC Sequence 25 AA;

Query Match 50.0%; Score 77; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renltrialy 25
 |||||
 QY 11 RENLRIALRY 20

RESULT 13

ID R95416 standard; peptide; 25 AA.
 AC R95416;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702.60-84.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLAB38.
 OS Synthetic.
 PN WO9528979-A1.
 PD 12-OCT-1995.
 PR 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Farham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 13: Page 32: 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLAB38. These sequences can be used to extend the period of acceptance
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides
 CC are administered to a patient in conjunction with a subtherapeutic amount
 CC of an immunosuppressant. This is administered to the patient for a
 CC limited period of time (compared to the lifetime administration for
 CC current treatments). The peptides particularly modulate (or inhibit) the
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
 SQ Sequence 25 AA:

Query Match 50.0%; Score 77; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renlrialy 25
 |||||
 Qy 11 RENLRIALRY 20

Search completed: Thu May 22 08:33:50 1997
 Job time : 8 secs.

WISREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:35:52 1997; MasPar time 2.11 Seconds
Tabular output not generated. 120.401 Million cell updates/sec

Title: >US-08-653-294-36
Description: (1-12) from US08653294.pep
Perfect Score: 98
Sequence: 1 YRLAIRRLRY 12

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 28.088; Variance 37.415; scale 0.751

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|------------|-----------------------|-----------|
| 1 | 63 | 64.3 | 375 | HRMA_PSESY | HRMA PROTEIN. | 4.00e-01 |
| 2 | 57 | 58.2 | 281 | STRF_STRGR | STREPTOMYCIN BIOSYNTH | 5.20e+00 |
| 3 | 57 | 58.2 | 348 | HLAF_MACMU | HLA CLASS I HISTOCOMP | 5.20e+00 |
| 4 | 57 | 58.2 | 477 | BGL2_BACSU | PROBABLE BETA-GLUCOSI | 5.20e+00 |
| 5 | 56 | 57.1 | 495 | ACH3_BOVIN | NEURONAL ACETYLCHOLIN | 7.83e+00 |
| 6 | 56 | 57.1 | 496 | ACH3_CHICK | NEURONAL ACETYLCHOLIN | 7.83e+00 |
| 7 | 56 | 57.1 | 499 | ACH3_RAT | NEURONAL ACETYLCHOLIN | 7.83e+00 |
| 8 | 56 | 57.1 | 502 | ACH3_HUMAN | NEURONAL ACETYLCHOLIN | 7.83e+00 |
| 9 | 56 | 57.1 | 1151 | GRR1_YEAST | GRR1 PROTEIN. | 7.83e+00 |
| 10 | 55 | 56.1 | 212 | YCD4_YEAST | HYPOTHETICAL 23.6 KD | 1.17e+01 |
| 11 | 55 | 56.1 | 491 | ACHE_BOVIN | ACETYLCHOLINE RECEPTO | 1.17e+01 |
| 12 | 55 | 56.1 | 493 | ACHE_HUMAN | ACETYLCHOLINE RECEPTO | 1.17e+01 |
| 13 | 55 | 56.1 | 583 | RUB2_BRANA | RUBISCO SUBUNIT BINDI | 1.17e+01 |
| 14 | 55 | 56.1 | 844 | DN44_HUMAN | DNA LIGASE IV (EC 6.5 | 1.17e+01 |
| 15 | 55 | 56.1 | 1420 | AP04_MACMU | APOLIPOPROTEIN(A) (EC | 1.17e+01 |
| 16 | 54 | 55.1 | 298 | PT03_ACACA | MITOCHONDRIAL RIBOSOM | 1.74e+01 |
| 17 | 54 | 55.1 | 493 | ACHE_MOUSE | ACETYLCHOLINE RECEPTO | 1.74e+01 |
| 18 | 54 | 55.1 | 494 | ACHE_RAT | ACETYLCHOLINE RECEPTO | 1.74e+01 |
| 19 | 54 | 55.1 | 500 | ACHE_DROME | ACETYLCHOLINE RECEPTO | 1.74e+01 |
| 20 | 54 | 55.1 | 651 | YHUK_ECOLI | HYPOTHETICAL 73.1 KD | 1.74e+01 |
| 21 | 54 | 55.1 | 699 | PTGA_BACSU | PTS SYSTEM, GLUCOSE-S | 1.74e+01 |
| 22 | 54 | 55.1 | 850 | RN12_YEAST | RN12 PROTEIN. | 1.74e+01 |

| | | | | | | | |
|----|----|------|------|----|------------|-----------------------|----------|
| 23 | 54 | 55.1 | 880 | 8 | RPAL_SULAC | DNA-DIRECTED RNA POLY | 1.74e+01 |
| 24 | 54 | 55.1 | 1748 | 7 | POIR_ELV | RNA REPLICASE POLYPRO | 1.74e+01 |
| 25 | 53 | 54.1 | 334 | 1 | BI0B_BREFL | BIOTIN SYNTHETASE (EC | 2.58e+01 |
| 26 | 53 | 54.1 | 347 | 10 | VAL1_SLCV | ALL PROTEIN. | 2.58e+01 |
| 27 | 53 | 54.1 | 454 | 1 | ACH5_CHICK | NEURONAL ACETYLCHOLIN | 2.58e+01 |
| 28 | 53 | 54.1 | 508 | 7 | PGKD_TRYBB | PHOSPHOGLYCERATE KINA | 2.58e+01 |
| 29 | 53 | 54.1 | 547 | 6 | MERA_STAAD | MERCURIC REDUCTASE (E | 2.58e+01 |
| 30 | 53 | 54.1 | 622 | 1 | ACH4_CHICK | NEURONAL ACETYLCHOLIN | 2.58e+01 |
| 31 | 53 | 54.1 | 852 | 2 | CLPB_CORGL | CLPB PROTEIN. | 2.58e+01 |
| 32 | 53 | 54.1 | 959 | 6 | MSH1_YEAST | MUTS PROTEIN HOMOLOG | 2.58e+01 |
| 33 | 53 | 54.1 | 1281 | 6 | MDR3_CRIGR | MULTIDRUG RESISTANCE | 2.58e+01 |
| 34 | 53 | 54.1 | 1858 | 10 | VGNB_CPSMV | GENOME POLYPROTEIN B | 2.58e+01 |
| 35 | 53 | 54.1 | 3391 | 7 | POLG_DEN27 | GENOME POLYPROTEIN (C | 2.58e+01 |
| 36 | 53 | 54.1 | 3391 | 7 | POLG_DEN26 | GENOME POLYPROTEIN (C | 2.58e+01 |
| 37 | 52 | 53.1 | 122 | 8 | RL17_CHLTR | 50S RIBOSOMAL PROTEIN | 3.79e+01 |
| 38 | 52 | 53.1 | 161 | 11 | YD95_YEAST | HYPOTHETICAL 18.9 KD | 3.79e+01 |
| 39 | 52 | 53.1 | 362 | 1 | 1B49_HUMAN | HLA CLASS I HISTOCOMP | 3.79e+01 |
| 40 | 52 | 53.1 | 362 | 1 | 1B62_HUMAN | HLA CLASS I HISTOCOMP | 3.79e+01 |
| 41 | 52 | 53.1 | 362 | 1 | 1B52_HUMAN | HLA CLASS I HISTOCOMP | 3.79e+01 |
| 42 | 52 | 53.1 | 473 | 1 | BGLB_MICBI | THERMOSTABLE BETA-GLU | 3.79e+01 |
| 43 | 52 | 53.1 | 609 | 7 | PRXC_CURIN | VANADIUM CHLOROPEROXI | 3.79e+01 |
| 44 | 52 | 53.1 | 682 | 7 | PRC_ECOLI | TAIL-SPECIFIC PROTEAS | 3.79e+01 |
| 45 | 52 | 53.1 | 948 | 7 | PMA3_ARATH | PLASMA MEMBRANE ATPAS | 3.79e+01 |

ALIGNMENTS

RESULT 1
ID HRMA_PSESY STANDARD; PRT; 375 AA.
AC Q08370;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DE 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HRMA PROTEIN.
GN HRMA.
OS PSEUDOMONAS SYRINGAE (PV. SYRINGAE).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC PSEUDOMONADACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PSS61;
RA HUANG H.C., HUTCHESON S.W., COLLIER A.;
RL MOL. PLANT MICROBE INTERACT. 4:469-476(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PSS61;
RX MEDLINE; 94100578.
RA HEU S., HUTCHESON S.W.;
RL MOL. PLANT MICROBE INTERACT. 6:553-564(1993).
CC -!- FUNCTION: UNKNOWN. MAY SERVE A REGULATORY FUNCTION.
DR EMBL; L14926; G294367;
KW HYPERSENSITIVE RESPONSE.
SQ SEQUENCE 375 AA; 41458 MW; 733EB06 CRC32;

Query Match 64.3%; Score 63; DB 5; Length 375;
Best Local Similarity 58.3%; Pred No. 4.00e-01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 174 yr1sitrk1sly 185
OY 1 YRLAIRRLRY 12

RESULT 2
ID STRF_STRGR STANDARD; PRT; 281 AA.
AC P09397;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE STREPTOMYCIN BIOSYNTHESIS PROTEIN STRF.
GN STRF.
OS STREPTOMYCES GRISEUS.
OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2-3-11;
 RX MEDLINE; 91375432.
 RA MANSOURI K., PIEPERSBERG W.;
 RL MOL. GEN. GENET. 228:459-469(1991).
 CC -!- FUNCTION: MAY BE INVOLVED IN THE FORMATION OF N-METHYL-L-
 CC GLUCOSAMINE.
 CC -!- PATHWAY: STREPTOMYCIN BIOSYNTHESIS.
 CC -!- SIMILARITY: LOW, TO THE AMINO-TERMINAL DOMAIN OF GLUCOSE-6-
 CC PHOSPHATE ISOMERASE.
 DR EMBL; Y00459; E11412; ALT_INIT.
 DR PIR; S17776; S17776.
 KW STREPTOMYCIN BIOSYNTHESIS.
 SQ SEQUENCE 281 AA; 31726 MW; 75CEB24C CRC32;
 Query Match 58.2%; Score 57; DB 9; Length 281;
 Best Local Similarity 70.0%; Pred. No. 5.20e+00;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 234 rlaarllamr 243
 QY 2 RLAIIRIALR 11
 RESULT 3
 ID HLA_F MACMU STANDARD; PRT; 348 AA.
 AC P33617;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F ALPHA CHAIN PRECURSOR (HLA F
 DE ANTIGEN) (LEUKOCYTE ANTIGEN F).
 GN HLA_F.
 OS MACACA MULATTA (RHESUS MACAQUE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93246295.
 RA OTTING N., BONTROP R.E.;
 RL IMMUNOGENETICS 38:141-145(1993).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 DR EMBL; Z21819; G38569; -;
 DR PIR; S29990; S29990.
 DR HSSP; P03989; 1HSA.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 21
 FT CHAIN 22 348
 FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN F.
 FT DOMAIN 22 113
 FT DOMAIN 114 205
 FT DOMAIN 206 297
 FT DOMAIN 298 307
 FT TRANSMEM 308 331
 FT DOMAIN 332 348
 FT DISULFID 124 187
 FT DISULFID 226 282
 FT CARBOHYD 109 109
 FT SEQUENCE 348 AA; 39300 MW; 3A375142 CRC32;
 Query Match 58.2%; Score 57; DB 5; Length 348;
 Best Local Similarity 54.5%; Pred. No. 5.20e+00;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 98 rvaalrllly 108
 QY 2 RLAIIRIALR 12

RESULT 4
 ID BGL2_BACSU STANDARD; PRT; 477 AA.
 AC P42403;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PROBABLE BETA-GLUCOSIDASE (EC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE)
 DE (BETA-D-GLUCOSIDE GLUCOHYDROLASE) (AMYGALASE).
 GN YCKE.
 OS BACILLUS SUBTILIS.
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE; 95219080.
 RA FUJISHIMA Y., YAMANE K.;
 RL MICROBIOLOGY 141:277-279(1995).
 RN [2]
 RP SEQUENCE OF 461-477 FROM N.A.
 RX MEDLINE; 88298684.
 RA VOSMAN B., KUIKEN G., KOOISTRA J., VENEMA G.;
 RL J. BACTERIOL. 170:3703-3710(1988).
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
 CC GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
 DR EMBL; D30762; G710632; -;
 DR EMBL; M21672; -; NOT_ANNOTATED_CDS.
 DR SUBTILIST; BG1181; YCKE.
 DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1.1.
 DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1.2.
 KW HYPOTHETICAL PROTEIN; HYDROLASE; GLYCOSIDASE; CELLULOSE DEGRADATION.
 FT ACT-SITE 170 170
 FT ACT-SITE 378 378
 FT SEQUENCE 477 AA; 55140 MW; E92CD679 CRC32;
 Query Match 58.2%; Score 57; DB 1; Length 477;
 Best Local Similarity 54.5%; Pred. No. 5.20e+00;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Db 360 rlgllrrlrry 370
 QY 2 RLAIIRIALR 12
 RESULT 5
 ID ACH3_BOVIN STANDARD; PRT; 495 AA.
 AC Q07263;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92319195.
 RA CRIADO M., ALAMO L., NAVARRO A.;
 RL NEUROCHEM. RES. 17:281-287(1993).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
 CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL; X57032; G237763; -;
 DR PROSITE; PS00236; NEUROTRN_ION_CHANNEL.
 KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
 KW TRANSMEMBRANE; MULTIGENE FAMILY.
 FT SIGNAL 1 21
 FT POTENTIAL.

FT CHAIN 22 495 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.
 FT DOMAIN 22 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 255 POTENTIAL.
 FT TRANSMEM 263 281 POTENTIAL.
 FT TRANSMEM 296 318 POTENTIAL.
 FT DOMAIN 319 467 CYTOPLASMIC (BY SIMILARITY).
 FT TRANSMEM 468 487 POTENTIAL.
 FT DISULFID 149 163 BY SIMILARITY.
 FT DISULFID 213 214 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 FT CARBOHYD 45 45 POTENTIAL.
 FT CARBOHYD 162 162 POTENTIAL.
 SQ SEQUENCE 495 AA; 56914 MW; 63BE4C2E CRC32;

Query Match 57.1%; Score 56; DB 1; Length 495;
 Best Local Similarity 58.3%; Pred. No. 7.83e+00;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 223 yslirrlply 234
 | | | | | | | | | |
 QY 1 YRLAIRRLRY 12

RESULT 6
 ID ACH3_CHICK STANDARD; PRT; 496 AA.
 AC P09481;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91009210.
 RA COUTURIER S., ERKMAN L., VALERA S., RUNGGER D., BERTRAND S.,
 RA BOULTER J., BALLIVET M., BERTRAND D.,
 RL J. BIOL. CHEM. 265:17560-17567(1990).
 RN [2]
 RP SEQUENCE OF 81-496 FROM N.A.
 RX MEDLINE; 88283624.
 RA NEF P., ONEYSER C., ALLIOT C., COUTURIER S., BALLIVET M.;
 RL EMO J. 7:595-601(1988).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
 CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
 CC FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
 CC THREE NON-ALPHA CHAINS.
 CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS IN THE DEVELOPING CILIARY AND
 CC SUPERIOR CERVICAL GANGLIA.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL; M37336; G211045; -;
 DR EMBL; X07345; G871036; -;
 DR EMBL; X07346; G871036; JOINED.
 DR EMBL; X07347; G871036; JOINED.
 DR PIR; S00378; ACCH3N.
 DR PROSITE; PS00236; NEUOTR_ION_CHANNEL.
 KW POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
 KW TRANSMEMBRANE; MULTIGENE FAMILY.
 FT SIGNAL 1 22
 FT CHAIN 23 496 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.
 FT DOMAIN 23 231 EXTRACELLULAR.
 FT TRANSMEM 232 256
 FT TRANSMEM 264 282
 FT TRANSMEM 298 319
 FT DOMAIN 320 468
 FT TRANSMEM 469 488 CYTOPLASMIC.
 FT DISULFID 150 164 BY SIMILARITY.

FT DISULFID 214 215 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 FT CARBOHYD 46 46 POTENTIAL.
 FT CARBOHYD 163 163 PROBABLE.
 SQ SEQUENCE 496 AA; 57027 MW; 883D3EA9 CRC32;
 Query Match 57.1%; Score 56; DB 1; Length 496;
 Best Local Similarity 58.3%; Pred. No. 7.83e+00;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 224 yslirrlply 235
 | | | | | | | | | |
 QY 1 YRLAIRRLRY 12

RESULT 7
 ID ACH3_RAT STANDARD; PRT; 499 AA.
 AC P04757;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.
 GN ACRA3.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86118671.
 RA BOULTER J., EVANS K., GOLDMAN D., MARTIN G., TRECO D., HEINEMANN S.,
 RA PATRICK J.;
 RL NATURE 319:368-374(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88041184.
 RA BOULTER J., CONNOLLY J., DENERIS E.S., GOLDMAN D.J., HEINEMANN S.F.,
 RA PATRICK J.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:7763-7767(1987).
 RN [3]
 RP SEQUENCE OF 1-21 FROM N.A.
 RX TISSUE-LIVER;
 RX MEDLINE; 94193711.
 RA YANG X., MCDONOUGH J., FYODOROV D., MORRIS M., WANG F.,
 RA DENERIS E.S.;
 RL J. BIOL. CHEM. 269:10252-10264(1994).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE
 CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL; X03440; G758258; -;
 DR EMBL; L31621; G468916; -;
 DR EMBL; U04961; G484069; -;
 DR PIR; A24572; A24572.
 DR PROSITE; PS00236; NEUOTR_ION_CHANNEL.
 KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
 KW TRANSMEMBRANE; MULTIGENE FAMILY.
 FT SIGNAL 1 25
 FT CHAIN 26 499 POTENTIAL.
 FT DOMAIN 26 234 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.
 FT TRANSMEM 235 259 EXTRACELLULAR.
 FT TRANSMEM 267 285
 FT TRANSMEM 301 322
 FT DOMAIN 323 471 CYTOPLASMIC.
 FT TRANSMEM 472 491
 FT DISULFID 153 167 BY SIMILARITY.
 FT DISULFID 217 218 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 FT CARBOHYD 49 49 POTENTIAL.

FT CARBOHYD 166 166 PROBABLE.
SQ SEQUENCE 499 AA; 56997 MW; E561713C CRC32;

Query Match 57.1%; Score 56; DB 1; Length 499;

Best Local Similarity 58.3%; Pred. No. 7.83e+00; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3;

Db 227 ysllyrrlplfy 238
| | | | | | | |
QY 1 YRLAIRRIALRY 12

RESULT 8
ID ACH3_HUMAN STANDARD; PRT; 502 AA.
AC P3297;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.
GN CHRNA3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90245296.
RA FORNASARI D., CHINI B., TARRONI P., CLEMENTI F.;
RL NEUROSCI. LETT. 111:351-356(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RX MEDLINE; 91114756.
RA MIHOVILOVIC M., ROSES A.D.;
RL EXP. NEUROL. 111:175-180(1991).
RN [3]
RP SEQUENCE OF 29-502 FROM N.A.
RC TISSUE=BRIN;
RA ANAND R., LINDSTROM J.;
RL SUBMITTED (JUN-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; M86383; G177898; -;
DR EMBL; X52239; G35090; -;
DR EMBL; M37981; G189253; -;
DR EMBL; X53559; G34986; -;
DR PIR; A37040; A37040;
DR PIR; S24595; S24595.
DR MIM; I18503; -;
KW PROSITE; PS00236; NEUROTR_ION_CHANNEL.
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
KW TRANSMEMBRANE; MULTIGENE FAMILY.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 502 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.
FT DOMAIN 29 237 EXTRACELLULAR.
FT TRANSMEM 238 262
FT TRANSMEM 270 288
FT TRANSMEM 304 325
FT DOMAIN 326 474
FT TRANSMEM 475 494 CYTOPLASMIC.
FT DISULFID 136 170
FT DISULFID 220 221 BY SIMILARITY.
FT CARBOHYD 52 52 ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
FT CARBOHYD 169 169 POTENTIAL.
FT CONFLICT 5 13 VSLPLACRA -> ALAAPCAVAP (IN REF. 2).
FT CONFLICT 99 99 D -> G (IN REF. 1).
FT CONFLICT 131 132 DD -> TT (IN REF. 1).

FT CONFLICT 234 234 I -> S (IN REF. 1).
FT CONFLICT 429 429 L -> V (IN REF. 1).
SQ SEQUENCE 502 AA; 57245 MW; 75D79DEC CRC32;

Query Match 57.1%; Score 56; DB 1; Length 502;

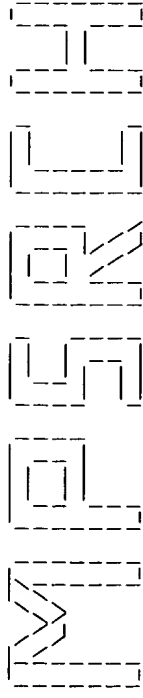
Best Local Similarity 58.3%; Pred. No. 7.83e+00; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 3;

Db 230 ysllyrrlplfy 241
| | | | | | | |
QY 1 YRLAIRRIALRY 12

RESULT 9
ID GRR1_YEAST STANDARD; PRT; 1151 AA.
AC P24814;
DT 01-NAR-1992 (REL. 21, CREATED)
DT 01-NAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE GRR1 PROTEIN.
GN GRR1 OR COT2 OR CAT80 OR YJR090C OR J1885.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92017785.
RA FLICK J.S., JOHNSTON M.;
RL MOL. CELL. BIOL. 11:5101-5112(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE; 96437976.
RA HUANG M.-E., MANUS V., CHUAT J.-C., GALIBERT F.;
RL YEAST 12:869-875(1996).
CC -!- FUNCTION: PROBABLY CONSTITUTES THE PRIMARY RESPONSE ELEMENT REQUIRED FOR THE GENERATION OR INTERPRETATION OF THE SIGNAL THAT INDUCES GLUCOSE REPRESSION. IS NOT AN ESSENTIAL PROTEIN.
CC -!- PATHWAY: NECESSARY FOR THE GLUCOSE REPRESSION PATHWAY.
CC -!- INDUCTION: IS EXPRESSED CONSTITUTIVELY AT LOW LEVELS.
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH THE PARTICULATE FRACTION. PROBABLY FORMS A COMPLEX BY PROTEIN-PROTEIN INTERACTIONS VIA ITS LEUCINE-RICH SEGMENT.
CC -!- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 12.
DR EMBL; M59247; G171617; -;
DR EMBL; Z49590; G1015784; -;
DR EMBL; L47993; G1019709; -;
DR PIR; A41529; A41529.
DR SGD; L0000730; GRR1.
DR LISTA; SC00406; GRR1.
KW GLUCOSE METABOLISM; REPEAT; LEUCINE-REPEAT.
FT DOMAIN 38 49 POLY-ASN.
FT DOMAIN 1045 1124 ASN-RICH.
FT DOMAIN 409 726 LEUCINE-RICH REPEATS.
FT REPEAT 409 434 LRR 1.
FT REPEAT 435 460 LRR 2.
FT REPEAT 461 486 LRR 3.
FT REPEAT 487 512 LRR 4.
FT REPEAT 513 548 LRR 5.
FT REPEAT 549 567 LRR 6.
FT REPEAT 568 593 LRR 7.
FT REPEAT 594 619 LRR 8.
FT REPEAT 620 645 LRR 9.
FT REPEAT 646 670 LRR 10.
FT REPEAT 671 699 LRR 11.
FT REPEAT 700 726 LRR 12.
SQ SEQUENCE 1151 AA; 132733 MW; 8C0DF89 CRC32;

Query Match 57.1%; Score 56; DB 4; Length 1151;
Best Local Similarity 41.7%; Pred. No. 7.83e+00; Indels 0; Gaps 0;
Matches 5; Conservative 4; Mismatches 3;

Db 386 yrlmikrinf 397



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:31:36 1997; MasPar time 2.71 Seconds
63.082 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-7
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 YRLAIR 6

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r50
1:ann1 2:ann2 3:ann3 4:ann4 5:ann11 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 21.577; Variance 27.148; scale 0.795

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description | Pred. No. |
|------------|-------|---------------|--------|----|-----------------------------|-----------|
| 1 | 47 | 95.9 | 388 | 16 | S15593 hypothetical protein | 7.12e+00 |
| 2 | 46 | 93.9 | 245 | 10 | D49898 cellobiose phosphotr | 1.13e+01 |
| 3 | 46 | 93.9 | 1330 | 11 | A36373 hypothetical protein | 1.13e+01 |
| 4 | 46 | 93.9 | 1333 | 11 | JN0791 Tf2 protein, Retrotr | 1.13e+01 |
| 5 | 45 | 91.8 | 1132 | 4 | QSBPL host specificity pro | 1.78e+01 |
| 6 | 45 | 91.8 | 2616 | 12 | A57096 nudel protein precu | 1.78e+01 |
| 7 | 45 | 91.8 | 3229 | 12 | S27852 hypothetical protein | 1.78e+01 |
| 8 | 45 | 91.8 | 3229 | 12 | A48450 probable cell-surfac | 1.78e+01 |
| 9 | 44 | 89.8 | 545 | 11 | JN0448 t-complex polypeptid | 2.79e+01 |
| 10 | 44 | 89.8 | 772 | 8 | JC4696 alpha.alpha.trehalos | 2.79e+01 |
| 11 | 44 | 89.8 | 883 | 12 | S31175 hypothetical protein | 2.79e+01 |
| 12 | 43 | 87.8 | 297 | 7 | B42144 ribosomal protein L5 | 4.33e+01 |
| 13 | 43 | 87.8 | 1603 | 1 | BVASAL aram protein - Emeri | 4.33e+01 |
| 14 | 42 | 85.7 | 83 | 4 | WBPT3 gene 18.7 protein - | 6.68e+01 |
| 15 | 42 | 85.7 | 223 | 16 | D49804 p25, Cp-capsid prote | 6.68e+01 |
| 16 | 42 | 85.7 | 256 | 1 | S10164 fumarate reductase (| 6.68e+01 |
| 17 | 42 | 85.7 | 268 | 9 | D64165 hypothetical protein | 6.68e+01 |
| 18 | 42 | 85.7 | 375 | 8 | A31383 hypothetical 40K pro | 6.68e+01 |
| 19 | 42 | 85.7 | 616 | 8 | B33586 C4-dicarboxylate tra | 6.68e+01 |
| 20 | 42 | 85.7 | 629 | 12 | S60385 probable membrane pr | 6.68e+01 |
| 21 | 42 | 85.7 | 938 | 14 | S11276 alpha-adaptin c - ra | 6.68e+01 |

| | | | | | | |
|----|----|------|------|----|------------------------------|----------|
| 22 | 42 | 85.7 | 938 | 14 | B30111 alpha-adaptin C - mo | 6.68e+01 |
| 23 | 42 | 85.7 | 977 | 14 | A30111 alpha-adaptin A - mo | 6.68e+01 |
| 24 | 42 | 85.7 | 1536 | 4 | RGBVS3 regulatory protein S | 6.68e+01 |
| 25 | 42 | 85.7 | 1692 | 11 | A33988 adenylate cyclase (E | 6.68e+01 |
| 26 | 42 | 85.7 | 2035 | 9 | A48654 high-molecular-weight | 6.68e+01 |
| 27 | 41 | 83.7 | 349 | 7 | S53023 nitrogen regulatory | 1.02e+02 |
| 28 | 41 | 83.7 | 353 | 4 | F2MWD1 photosystem II D1 pr | 1.02e+02 |
| 29 | 41 | 83.7 | 360 | 16 | A48306 photosystem II D1 pr | 1.02e+02 |
| 30 | 41 | 83.7 | 360 | 7 | S45009 D1 subunit of photos | 1.02e+02 |
| 31 | 41 | 83.7 | 360 | 7 | S26586 photosystem II prote | 1.02e+02 |
| 32 | 41 | 83.7 | 360 | 7 | S32576 photosystem II prote | 1.02e+02 |
| 33 | 41 | 83.7 | 360 | 7 | S54256 photosystem II prote | 1.02e+02 |
| 34 | 41 | 83.7 | 360 | 7 | S23362 photosystem II prote | 1.02e+02 |
| 35 | 41 | 83.7 | 360 | 7 | S32577 photosystem II prote | 1.02e+02 |
| 36 | 41 | 83.7 | 360 | 4 | F2A117 photosystem II prote | 1.02e+02 |
| 37 | 41 | 83.7 | 445 | 11 | S59646 hypothetical protein | 1.02e+02 |
| 38 | 41 | 83.7 | 481 | 10 | S47441 transport protein ert | 1.02e+02 |
| 39 | 41 | 83.7 | 583 | 6 | S17671 protein-tyrosine-pho | 1.02e+02 |
| 40 | 41 | 83.7 | 626 | 16 | S34120 DNA-directed DNA pol | 1.02e+02 |
| 41 | 41 | 83.7 | 732 | 1 | S07624 acylaminoacyl-peptid | 1.02e+02 |
| 42 | 41 | 83.7 | 732 | 13 | JC4655 acylaminoacyl-peptid | 1.02e+02 |
| 43 | 41 | 83.7 | 768 | 5 | S19263 DNA-directed DNA pol | 1.02e+02 |
| 44 | 41 | 83.7 | 783 | 1 | JDEC22 DNA-directed DNA pol | 1.02e+02 |
| 45 | 41 | 83.7 | 1997 | 6 | S12050 protein-tyrosine-pho | 1.02e+02 |

ALIGNMENTS

RESULT 1
ENTRY S15593 #type complete
TITLE hypothetical protein (insertion sequence ISH27-3) -
ORGANISM Halobacterium halobium
DATE 21-Nov-1993 #sequence_revision 21-Nov-1993 #text_change
ACCESSIONS S15593
REFERENCE Pfeifer, F.; Blaselo, U.
#authors Nucleic Acids Res. (1990) 18:6921-6925
#journal Transposition Burst of the ISH27 insertion element family in
#title Halobacterium halobium.
#cross-references MUID:91088266
#accession S15593 preliminary
#status 1-388 #label PFE
#residues
#cross-references EMBL:X5434
SUMMARY #length 388 #molecular-weight 44571 #checksum 1952

Query Match 95.9% Score 47; DB 16; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.12e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 154 yrlavr 159
| | | | |
QY 1 YRLAIR 6

RESULT 2
ENTRY D49898 #type complete
TITLE cellobiose phosphotransferase system cels - Bacillus
ORGANISM steartothermophilus
DATE 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change

ACCESSIONS D49898
REFERENCE J. Bacteriol. (1993) 175:6441-6450
#authors Lai, X.; Ingram, L.O.
#journal Cloning and sequencing of a cellobiose phosphotransferase
#title system operon from Bacillus steartothermophilus XL-65-6 and
functional expression in Escherichia coli.
#cross-references MUID:94012514
#contents XL-65-6

```

#accession D49898
#status preliminary
#molecule_type DNA
#residues 1-245 #label LAI
#note sequence extracted from NCBI backbone
SUMMARY #length 245 #molecular-weight 27430 #checksum 647

Query Match 93.9%; Score 46; DB 10; Length 245;
Best Local Similarity 83.3%; Pred. No. 1.13e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 142 yrlpir 147
|||:|
QY 1 YRLAIR 6

RESULT 3
ENTRY #type complete
TITLE hypothetical protein Tfl - fission yeast (Schizosaccharomyces
ORGANISM pombe)
#formal_name Schizosaccharomyces pombe
DATE 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change
30-Sep-1993
ACCESSIONS A36373
REFERENCE A36373
#authors Levin, H.L.; Weaver, D.C.; Boeke, J.D.
#journal Mol. Cell. Biol. (1990) 10:6791-6798
#title Two related families of retrotransposons from
Schizosaccharomyces pombe.
#cross-references MUID:91061791
#accession A36373
#status preliminary
#molecule_type DNA
#residues 1-1330 #label LEV
#cross-references GB:M38526
SUMMARY #length 1330 #molecular-weight 154795 #checksum 1686

Query Match 93.9%; Score 46; DB 11; Length 1330;
Best Local Similarity 83.3%; Pred. No. 1.13e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 408 yrlpir 413
|||:|
QY 1 YRLAIR 6

RESULT 4
ENTRY #type complete
TITLE Tf2 protein, Retrotransposon - fission yeast
(Schizosaccharomyces pombe)
ORGANISM #formal_name Schizosaccharomyces pombe
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change
03-May-1994
ACCESSIONS JN0791
REFERENCE JN0791
#authors Weaver, D.C.; Shpakovski, G.V.; Caputo, E.; Levin, H.L.;
Boeke, J.D.
#journal Gene (1993) 131:135-139
#title Sequence analysis of closely related retrotransposon families
from fission yeast.
#accession JN0791
#molecule_type DNA
#residues 1-1333 #label WEA
#cross-references GB:L10324
GENETICS
#gene Tf2
SUMMARY #length 1333 #molecular-weight 154915 #checksum 3353

Query Match 93.9%; Score 46; DB 11; Length 1333;
Best Local Similarity 83.3%; Pred. No. 1.13e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 411 yrlpir 416
|||:|
QY 1 YRLAIR 6

RESULT 5
ENTRY #type complete
TITLE host specificity protein J - phage lambda
ORGANISM #formal_name phage lambda
DATE 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change
31-Dec-1993
ACCESSIONS D43009; A43015; A04374
REFERENCE A94614
#authors Daniels, D.
#submission submitted to the Nucleic Acid Sequence Database, September
1982
#accession D43009
#molecule_type DNA
#residues 1-1132 #label DAN
REFERENCE A92891
#authors Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen,
G.B.
#journal J. Mol. Biol. (1982) 162:729-773
#title Nucleotide sequence of bacteriophage lambda DNA.
#cross-references MUID:83189071
#accession A43015
#molecule_type DNA
#residues 1-1132 #label SAN
COMMENT Gene J protein makes up the distal fiber of the phage tail. It is
responsible for adsorption to the host during infection and
determines host specificity. It specifically binds to the lambda
receptor protein of E. coli K12. This receptor protein encoded by
E. coli gene lamB is an outer membrane protein that functions in
the transport of maltose and maltodextrins.
COMMENT Under the action of the gene G, T, H, M, L, K, and I proteins, gene
J protein serves as the initiator of tail polymerization. There
are 2-4 copies of protein J per mature phage.
GENETICS
#gene J
#map_position 31.97-38.97
CLASSIFICATION #superfamily phage lambda host specificity protein J
SUMMARY #length 1132 #molecular-weight 124421 #checksum 1868

Query Match 91.8%; Score 45; DB 4; Length 1132;
Best Local Similarity 66.7%; Pred. No. 1.78e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 688 yrltvr 693
|||:|
QY 1 YRLAIR 6

RESULT 6
ENTRY #type complete
TITLE nudel protein precursor - fruit fly (Drosophila melanogaster)
ORGANISM #formal_name Drosophila melanogaster
DATE 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change
19-Jan-1996
ACCESSIONS A57096
REFERENCE A57096
#authors Hong, C.C.; Hashimoto, C.
#journal Cell (1995) 82:785-794
#title An unusual mosaic protein with a protease domain, encoded by
the nudel gene, is involved in defining embryonic
dorsoventral polarity in Drosophila.
#accession A57096
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-2616 #label HON
#cross-references GB:U29153
CLASSIFICATION #superfamily LDL receptor ligand-binding repeat homology
KEYWORDS extracellular protein
FEATURE

```

```

891-929      #domain LDL receptor ligand-binding repeat homology
2421-2457    #label LDL1\
             #domain LDL receptor ligand-binding repeat homology
             #label LDL3
SUMMARY      #length 2616 #molecular-weight 292372 #checksum 9962

Query Match      91.8%; Score 45; DB 12; Length 2616;
Best Local Similarity 83.3%; Pred. No. 1.78e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2609 yrleir 2614
||| ||
QY 1 YRLAIR 6

RESULT 7
ENTRY      S27852      #type complete
TITLE      hypothetical protein DGF-1 - Trypanosoma cruzi
ORGANISM    #formal_name Trypanosoma cruzi
DATE        17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
30-Sep-1993
ACCESSIONS  S27852
REFERENCE    #authors Wincker, P.; Murta-Dovales, A.C.; Goldenberg, S.
             #submission submitted to the EMBL Data Library, April 1992
             #description Nucleotide sequence of a representative member of a
             Trypanosoma cruzi dispersed gene family.
             #accession S27852
             #molecule_type DNA
             #residues 1-3229 #label WIN
             #cross-references EMBL:M90534
SUMMARY      #length 3229 #molecular-weight 334929 #checksum 5768

Query Match      91.8%; Score 45; DB 12; Length 3229;
Best Local Similarity 66.7%; Pred. No. 1.78e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1266 yrleir 1271
||| ||
QY 1 YRLAIR 6

RESULT 8
ENTRY      A48450      #type complete
TITLE      probable cell-surface protein (cysteine-rich repeat motif) -
             Trypanosoma cruzi
ORGANISM    #formal_name Trypanosoma cruzi
DATE        01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
03-Mar-1995
ACCESSIONS  A48450
REFERENCE    #authors Wincker, P.; Murto-Dovales, A.C.; Goldenberg, S.
             #journal Mol. Biochem. Parasitol. (1992) 55:217-220
             #title Nucleotide sequence of a representative member of a
             Trypanosoma cruzi dispersed gene family.
             #cross-references MUID:93063053
             #accession A48450
             #status preliminary; not compared with conceptual translation
             #molecule_type DNA
             #residues 1-3229 #label WIN
             #cross-references NCBI:P118407
             #note sequence extracted from NCBI backbone
SUMMARY      #length 3229 #molecular-weight 334929 #checksum 5768

Query Match      91.8%; Score 45; DB 12; Length 3229;
Best Local Similarity 66.7%; Pred. No. 1.78e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1266 yrleir 1271
||| ||
QY 1 YRLAIR 6

```

```

RESULT 9
ENTRY      JN0448      #type complete
TITLE      t-complex polypeptide Tcpl-1 - Arabidopsis thaliana
ORGANISM    #formal_name Arabidopsis thaliana #common_name mouse-ear
             cress
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
30-Sep-1993
ACCESSIONS  JN0448
REFERENCE    #authors Mori, M.; Murata, K.; Kubota, H.; Yamamoto, A.; Matsushiro,
             A.; Morita, T.
             #journal Gene (1992) 122:381-382
             #title Cloning of a cDNA encoding the Tcpl-1 (t complex polypeptide
             1) homologue of Arabidopsis thaliana.
             #accession JN0448
             #molecule_type mRNA
             #residues 1-545 #label MOR
             #cross-references DDBJ:D11351
SUMMARY      #length 545 #molecular-weight 59229 #checksum 1573

Query Match      89.8%; Score 44; DB 11; Length 545;
Best Local Similarity 83.3%; Pred. No. 2.79e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 124 yrleir 129
||| ||
QY 1 YRLAIR 6

RESULT 10
ENTRY      JC4696      #type complete
TITLE      alpha, alpha-trehalose-phosphate synthase (EC 2.4.1.-) -
             Rhizobium sp.
ORGANISM    #formal_name Rhizobium sp.
DATE        10-May-1996 #sequence_revision 19-Jul-1996 #text_change
19-Jul-1996
ACCESSIONS  JC4696
REFERENCE    #authors Maruta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto,
             T.; Kurimoto, M.
             #journal Biosci. Biotechnol. Biochem. (1996) 60:717-720
             #title Cloning and sequencing of trehalose biosynthesis genes from
             Rhizobium sp. M-11.
             #accession JC4696
             #molecule_type DNA
             #residues 1-772 #label MAR
             #cross-references DDBJ:D78001
COMMENT      This enzyme belongs to alpha-amylase family. It catalyzes the
             conversion of maltodextrins to maltotriose and maltotetraose by
             forming alpha, alpha-1,1-glucosidic linkage by an intramolecular
             transglucosylation.

GENETICS
#gene
KEYWORDS    MTSase
SUMMARY      #length 772 #molecular-weight 84859 #checksum 8061

Query Match      89.8%; Score 44; DB 8; Length 772;
Best Local Similarity 83.3%; Pred. No. 2.79e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 8 yrleir 13
||| ||
QY 1 YRLAIR 6

RESULT 11
ENTRY      S31175      #type complete
TITLE      hypothetical protein 2 - midge (Chironomus thummi) transposon
             NLR1Cth
ORGANISM    #formal_name Chironomus thummi
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
30-Sep-1993
ACCESSIONS  S31175

```

```

REFERENCE S31174
#authors Blinov, A.G.; Sobanov, Y.V.; Bogachev, S.S.; Donchenko, A.P.;
#journal Filippova, M.A. (1993) 237:412-420
#title Mol. Gen. Genet. (1993) 237:412-420
#title The Chironomus thummi genome contains a non-LTR
retrotransposon.
#accession S31175
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-883 #label BLI
SUMMARY #length 883 #molecular-weight 102009 #checksum 5809
Query Match 89.8%; Score 44; DB 12; Length 883;
Best Local Similarity 83.3%; Pred. No. 2.79e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 803 yklair 808
QY 1 YRLAIR 6
RESULT 12
ENTRY S42144 #type complete
TITLE ribosomal protein L5.e - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein LPII4w; protein YPL131w; ribosomal protein YL1;
ribosomal protein YL3
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 03-May-1994 #sequence_revision 27-Jan-1995 #text_change
06-Sep-1996
ACCESSIONS S42144; S48089; S11574; S69053; A38724
REFERENCE S42144
#authors Deshmukh, M.; Tsay, Y.F.; Paulovich, A.G.; Woolford Jr., J.L.
#journal Mol. Cell. Biol. (1993) 13:2835-2845
#title Yeast ribosomal protein L1 is required for the stability of
newly synthesized 5S rRNA and the assembly of 60S ribosomal
subunits.
#accession S42144
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-297 #label DES
#cross-references EMBL:L01796
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1992
REFERENCE A38724
#authors Tang, B.; Nazar, R.N.
#journal J. Biol. Chem. (1991) 266:6120-6123
#title Structure of the yeast ribosomal 5 S RNA-binding protein YL3.
#cross-references MUID:91177855
#accession S14172
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-111,'R',113-297 #label TAN
REFERENCE S48088
#authors Tang, B.; Nazar, R.N.
#journal J. Biol. Chem. (1992) 267:17738-17742
#title Unbalanced regulation of the ribosomal 5 S RNA-binding
protein in Saccharomyces cerevisiae expressing mutant 5 S
rRNAs.
#accession S48089
#status translation not shown
#molecule_type DNA
#residues 1-111,'R',113-297 #label TA2
#cross-references EMBL:M94864
REFERENCE S11574
#authors Nazar, R.N.; Yaguchi, M.; Willick, G.E.; Rollin, C.F.; Roy,
C.
#journal Eur. J. Biochem. (1979) 102:573-582
#title The 5-S RNA binding protein from yeast (Saccharomyces
cerevisiae) ribosomes. Evolution of the eukaryotic 5-S RNA
binding protein.
#cross-references MUID:80112896
#accession S11574
#molecule_type protein

```

```

#residues 2-31;209-256 #label NAZ
#note the sequence from the summary and Fig. 5 is inconsistent
with that from tables 2 and 3 in having 17-Tyr
REFERENCE S69040
#authors Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.;
Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wang, Y.; Winnett,
E.
#submission submitted to the EMBL Data Library, December 1995
#description The sequence of saccharomyces cerevisiae chromosome XVI left
arm.
#accession S69053
#molecule_type DNA
#residues 1-297 #label HAL
#cross-references EMBL:U43703
GENETICS LISTA:RPL1
#gene
#map_position 16L
CLASSIFICATION #superfamily rat ribosomal protein L5
KEYWORDS protein biosynthesis; ribosome; RNA binding
FEATURE
2-297 #product ribosomal protein L5.e #status experimental
#label MAI
SUMMARY #length 297 #molecular-weight 33714 #checksum 4118
Query Match 87.8%; Score 43; DB 7; Length 297;
Best Local Similarity 66.7%; Pred. No. 4.33e+01;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 49 yrlvvr 54
QY 1 YRLAIR 6
RESULT 13
ENTRY BVAS1 #type complete
TITLE arom protein - Emericella nidulans
ALTERNATE_NAMES biosynthetic dehydroquinase
CONTAINS 3-dehydroquininate dehydratase (EC 4.2.1.10); 3-dehydroquininate
synthase (EC 4.6.1.3); 3-phosphoshikimate
1-carboxyvinyltransferase (EC 2.5.1.19); shikimate
5-dehydrogenase (EC 1.1.1.25); shikimate kinase (EC
2.7.1.71)
ORGANISM #formal_name Emericella nidulans, Aspergillus nidulans
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
18-Aug-1995
ACCESSIONS A24962; A24042
REFERENCE A24962
#authors Charles, I.G.; Keyte, J.W.; Brammar, W.J.; Smith, M.;
Hawkins, A.R.
#journal Nucleic Acids Res. (1986) 14:2201-2213
#title The isolation and nucleotide sequence of the complex AROM
locus of Aspergillus nidulans.
#cross-references MUID:86176723
#accession A24962
#molecule_type DNA
#residues 1-1603 #label DUN
REFERENCE A24042
#authors Charles, I.G.; Keyte, J.W.; Brammar, W.J.; Hawkins, A.R.
#journal Nucleic Acids Res. (1985) 13:8119-8128
#title Nucleotide sequence encoding the biosynthetic dehydroquinase
function of the penta-functional AROM locus of Aspergillus
nidulans.
#cross-references MUID:86067221
#accession A24042
#molecule_type DNA
#residues 844-1048,'G',1050-1093,'N',1095-1458,'T',1460-1474
#label CHA
GENETICS
#gene arom
CLASSIFICATION #superfamily aroI protein; 3-dehydroquininate dehydratase
homology; 3-dehydroquininate synthase homology;
3-phosphoshikimate 1-carboxyvinyltransferase homology;
shikimate dehydrogenase homology; shikimate kinase homology

```

KEYWORDS

aromatic amino acid biosynthesis; ATP binding; carbon-oxygen lyase; hydro-lyase; multifunctional enzyme; NADP; oxidoreductase; phosphorus-oxygen lyase; phosphotransferase; transferase

FEATURE

7-372 #domain 3-dehydroquinase synthase homology #label DQS\
407-835 #domain 3-phosphoshikimate 1-carboxyvinyltransferase homology #label PSK\
863-982 #domain shikimate kinase homology #label SKI\
1037-1277 #domain 3-dehydroquinase dehydratase homology #label DDD\
1344-1567 #domain shikimate dehydrogenase homology #label SKD

SUMMARY

#length 1603 #molecular-weight 175079 #checksum 7102

Query Match

Best Local Similarity 87.8%; Score 43; DB 1; Length 1603;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1141 yrlafr 1146

Y 1 YRLAIR 6

RESULT 14

ENTRY

W8BPT3 #type complete

gene 18.7 protein - phase T3

ORGANISM #formal_name phase T3

#note host Escherichia coli

DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 07-Apr-1994

ACCESSIONS

E23476

REFERENCE

A94339

#authors Yamada, M.; Fujisawa, H.; Kato, H.; Hamada, K.; Minagawa, T.

#journal Virology (1986) 151:350-361

#title Cloning and sequencing of the genetic right end of bacteriophage T3 DNA.

#cross-references MUID:86209997

#accession E23476

#molecule_type DNA

#residues 1-83 #label YAM

REFERENCE

A94344

#authors Yamada, M.; Fujisawa, H.; Kato, H.; Hamada, K.; Minagawa, T.

#journal Virology (1986) 154:246

#contents annotation; erratum; corrections to coding regions

GENETICS 18.7

#gene superfamily phase T7 gene 18.7 protein

CLASSIFICATION #length 83 #molecular-weight 9393 #checksum 4304

SUMMARY

Query Match 85.7%; Score 42; DB 4; Length 83;

Best Local Similarity 66.7%; Pred. No. 6.68e+01;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 20 yrlsik 25

Y 1 YRLAIR 6

RESULT 15

ENTRY

D49804 #type complete

p25, CP-capsid protein - citrus tristeza closterovirus CTV

ORGANISM #common_name citrus tristeza closterovirus CTV

DATE 11-Oct-1994 #sequence_revision 11-Oct-1994 #text_change 11-Oct-1994

ACCESSIONS

D49804

REFERENCE

A49804

#authors Pappu, H.R.; Karasev, A.V.; Anderson, E.J.; Pappu, S.S.;

Hilf, M.E.; Febres, V.J.; Eckloff, R.M.; McCaffery, M.;

Boyko, V.; Gowda, S.; Dolla, V.V.; Koonin, E.V.; Gumpf, D.J.; Cline, K.C.; Garnsey, S.M.; Dawson, W.O.; Lee, R.F.; Niblett, C.L.

Virology (1994) 199:35-46

#journal Nucleotide sequence and organization of eight 3' open reading

#title

#cross-references MUID:94160579
#contents 136, severe quick decline isolate
#accession D49804

##status preliminary

##molecule_type genomic RNA

##residues 1-223 #label PAP

##cross-references NCBIN:144092; NCBIP:144102

##note sequence extracted from NCBI backbone

SUMMARY #length 223 #molecular-weight 24890 #checksum 4316

Query Match

Best Local Similarity 85.7%; Score 42; DB 16; Length 223;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 85 yrlavk 90

Y 1 YRLAIR 6

Search completed: Thu May 22 08:31:55 1997

Job time : 19 secs.

THIS PAGE BLANK (USPTO)

WISREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelligentGenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:27:58 1997; MasPar time 1.97 Seconds

Tabular output not generated. 64.764 Million cell updates/sec

Title: >US-08-653-294-5
Description: (1-6) from US08653294.pep
Perfect score: 53
Sequence: 1 RILLRY 6

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 23.812; Variance 26.364; scale 0.903

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|---------------|-----------------------|-----------|
| 1 | 48 | 90.6 | 830 | HM1L_SCHPO | HEAVY METAL TOLERANCE | 5.28e+00 |
| 2 | 48 | 90.6 | 832 | 11 YC26_YEAST | PUTATIVE 95.7 KD TRAN | 5.28e+00 |
| 3 | 47 | 88.7 | 139 | 10 VPPE_HUMAN | IMMUNOGLOBULIN IOTA C | 8.61e+00 |
| 4 | 47 | 88.7 | 142 | 10 VPR1_MOUSE | IMMUNOGLOBULIN IOTA C | 8.61e+00 |
| 5 | 47 | 88.7 | 142 | 10 VPR2_MOUSE | IMMUNOGLOBULIN IOTA C | 8.61e+00 |
| 6 | 47 | 88.7 | 225 | 2 CBQI_SALTY | COBALT TRANSPORT PROT | 8.61e+00 |
| 7 | 47 | 88.7 | 496 | 6 MMSA_FSEAE | METHYLMALONATE-SEMIAL | 8.61e+00 |
| 8 | 46 | 86.8 | 328 | 4 HAIQ_MOUSE | H-2 CLASS I HISTOCOMP | 1.39e+01 |
| 9 | 46 | 86.8 | 338 | 1 IB20_HUMAN | HLA CLASS I HISTOCOMP | 1.39e+01 |
| 10 | 46 | 86.8 | 346 | 7 PP12_TRYBB | SERINE/THREONINE PROT | 1.39e+01 |
| 11 | 46 | 86.8 | 361 | 1 IB14_HUMAN | HLA CLASS I HISTOCOMP | 1.39e+01 |
| 12 | 46 | 86.8 | 362 | 4 HAI3_MOUSE | H-2 CLASS I HISTOCOMP | 1.39e+01 |
| 13 | 46 | 86.8 | 362 | 1 IB18_HUMAN | HLA CLASS I HISTOCOMP | 1.39e+01 |
| 14 | 46 | 86.8 | 362 | 1 IB45_HUMAN | HLA CLASS I HISTOCOMP | 1.39e+01 |
| 15 | 46 | 86.8 | 362 | 1 IB16_HUMAN | HLA CLASS I HISTOCOMP | 1.39e+01 |
| 16 | 46 | 86.8 | 362 | 1 IB29_HUMAN | HLA CLASS I HISTOCOMP | 1.39e+01 |
| 17 | 46 | 86.8 | 362 | 1 IB19_HUMAN | HLA CLASS I HISTOCOMP | 1.39e+01 |
| 18 | 46 | 86.8 | 365 | 6 MEXF_HUMAN | MYOCYTE-SPECIFIC ENHA | 1.39e+01 |
| 19 | 46 | 86.8 | 368 | 4 HAIW_MOUSE | H-2 CLASS I HISTOCOMP | 1.39e+01 |
| 20 | 46 | 86.8 | 411 | 6 LYOX_MOUSE | PROTEIN-LYSINE 6-OXID | 1.39e+01 |
| 21 | 46 | 86.8 | 411 | 6 LYOX_RAT | PROTEIN-LYSINE 6-OXID | 1.39e+01 |
| 22 | 46 | 86.8 | 417 | 6 LYOX_HUMAN | PROTEIN-LYSINE 6-OXID | 1.39e+01 |

| | | | | | | |
|----|----|------|------|---------------|-------------------------|----------|
| 23 | 46 | 86.8 | 420 | 6 LYOX_CHICK | PROTEIN-LYSINE 6-OXID | 1.39e+01 |
| 24 | 46 | 86.8 | 515 | 6 MEF2_DROME | MYOCYTE-SPECIFIC ENHA | 1.39e+01 |
| 25 | 46 | 86.8 | 1626 | 9 TOPB_HUMAN | DNA TOPOISOMERASE II, | 1.39e+01 |
| 26 | 45 | 84.9 | 217 | 9 TER4_ECOLI | TETRACYCLINE REPRESSO | 2.23e+01 |
| 27 | 45 | 84.9 | 218 | 9 TER8_PASPI | TETRACYCLINE REPRESSO | 2.23e+01 |
| 28 | 45 | 84.9 | 298 | 9 RT03_ACACA | MITOCHONDRIAL RIBOSOM | 2.23e+01 |
| 29 | 45 | 84.9 | 1203 | 9 SDC1_CABEL | ZINC FINGER PROTEIN S | 2.23e+01 |
| 30 | 44 | 83.0 | 168 | 11 YZDC_ECOLI | VERY HYPOTHETICAL 20. | 3.54e+01 |
| 31 | 44 | 83.0 | 217 | 11 YJ17_YEAST | HYPOTHETICAL 24.5 KD | 3.54e+01 |
| 32 | 44 | 83.0 | 338 | 4 GALE_NEIGO | UDP-GLUCOSE 4-EPIMERASE | 3.54e+01 |
| 33 | 44 | 83.0 | 402 | 11 YG34_YEAST | HYPOTHETICAL 45.3 KD | 3.54e+01 |
| 34 | 44 | 83.0 | 410 | 1 ATIN_VZVD | ALPHA TRANS-INDUCING | 3.54e+01 |
| 35 | 44 | 83.0 | 607 | 11 YN92_YEAST | PUTATIVE TRANSCRIPTIO | 3.54e+01 |
| 36 | 44 | 83.0 | 633 | 5 KS62_MOUSE | RIBOSOMAL PROTEIN S6 | 3.54e+01 |
| 37 | 44 | 83.0 | 724 | 5 KS61_MOUSE | RIBOSOMAL PROTEIN S6 | 3.54e+01 |
| 38 | 44 | 83.0 | 740 | 5 KS62_HUMAN | RIBOSOMAL PROTEIN S6 | 3.54e+01 |
| 39 | 44 | 83.0 | 752 | 5 KS6A_CHICK | RIBOSOMAL PROTEIN S6 | 3.54e+01 |
| 40 | 44 | 83.0 | 817 | 8 RRPO_CRV | PROBABLE RNA-DIRECTED | 3.54e+01 |
| 41 | 44 | 83.0 | 817 | 8 RRPO_TBSVC | PROBABLE RNA-DIRECTED | 3.54e+01 |
| 42 | 44 | 83.0 | 817 | 8 RRPO_CNV | PROBABLE RNA-DIRECTED | 3.54e+01 |
| 43 | 44 | 83.0 | 1174 | 11 YJ11_YEAST | HYPOTHETICAL 135.1 KD | 3.54e+01 |
| 44 | 44 | 83.0 | 1216 | 1 ATC2_YEAST | PROBABLE CALCIUM-TRAN | 3.54e+01 |
| 45 | 44 | 83.0 | 1741 | 8 RPL1_GIALA | DNA-DIRECTED RNA POLY | 3.54e+01 |

ALIGNMENTS

RESULT 1
ID HM1L_SCHPO STANDARD; PRT; 830 AA.
AC Q02592;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HEAVY METAL TOLERANCE PROTEIN PRECURSOR.
GN HM1L.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SP223;
RX MEDLINE; 93010938.
RA ORTIZ D.F., KREPEL L., SPEISER D.M., SCHEEL G., MCDONALD G.,
OW D.W.;
RL EMBO J. 11:3491-3499(1992).
CC -!- FUNCTION: INVOLVED IN METAL TOLERANCE. PROBABLY INVOLVED IN THE
TRANSPORT OF METAL-BOUND PHYTOCHELATIONS. COMPARTMENTALIZES
CADMIUM WITHIN VACUOLES, THEREBY PROTECTING CELLS FROM CADMIUM
TOXICITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. VACUOLAR.
CC -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.
CC EMBL; Z14055; G4972; -.
CC PIR; S25198; S25198.
DR PROSITE; PS00211; ABC_TRANSPORTER.
KW CADMIUM; METAL-BINDING; TRANSMEMBRANE; SIGNAL; ATP-BINDING;
KW GLYCOPROTEIN; CADMIUM RESISTANCE.
FT SIGNAL 1 27
FT CHAIN 28 830 HEAVY METAL TOLERANCE PROTEIN.
FT TRANSMEM 10 31 POTENTIAL.
FT TRANSMEM 52 71 POTENTIAL.
FT TRANSMEM 88 108 POTENTIAL.
FT TRANSMEM 126 146 POTENTIAL.
FT TRANSMEM 403 423 POTENTIAL.
FT TRANSMEM 490 511 POTENTIAL.
FT NP_BIND 617 624 ATP (POTENTIAL).
FT CARBOHYD 150 150 POTENTIAL.
FT CARBOHYD 350 350 POTENTIAL.
SQ SEQUENCE 830 AA; 94007 MW; 32AA6381 CRC32;

Query Match 90.6%; Score 48; DB 5; Length 830;
Best local similarity 83.3%; Pred. No. 5.28e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


```

RESULT 5
ID VPR2_MOUSE STANDARD; PRT; 142 AA.
AC P13373;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IMMUNOGLOBULIN OMEGA CHAIN PRECURSOR (V(PREB)2 PROTEIN).
GN VPREB2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2J X C57BL/6;
RX MEDLINE; 88029315.
RA KUDO A., MELCHERS F.;
RL EMBO J. 6:2267-2272(1987).
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC STEPS OF B-CELL DIFFERENTIATION.
CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
DR EMBL; X05563; G55416; -.
DR PIR; B28344; B28344.
DR HSSP; P01607; 1FGV.
KW IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 142 V(PREB)2 PROTEIN.
FT DOMAIN 20 41 FRAMEWORK 1.
FT DOMAIN 42 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 70 FRAMEWORK 2.
FT DOMAIN 71 81 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 82 115 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
SQ SEQUENCE 142 AA; 16052 MW; 6AE40A3B CRC32;

Query Match 88.7%; Score 47; DB 10; Length 142;
Best Local Similarity 83.3%; Pred. No. 8.61e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 56 rllry 71
   1:||||
Qy 1 RILLY 6

RESULT 6
ID CBIQ_SALTY STANDARD; PRT; 225 AA.
AC Q05598;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE COBALT TRANSPORT PROTEIN CBIQ.
GN CBIQ.
OS SALMONELLA TYPHIMURIUM.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LT2;
RX MEDLINE; 93273696.
RA ROTH J.R., LAWRENCE J.G., RUBENFELD M., KIEFFER-HIGGINS S.,
RA CHURCH G.M.;
RL J. BACTERIOL. 175:3303-3316(1993).
CC -!- FUNCTION: MAY BE INVOLVED WITH COBALT TRANSPORT IN ASSOCIATION
CC WITH COBALAMIN BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- PATHWAY: COBALAMIN BIOSYNTHESIS.
DR EMBL; L12006; G154434; -.
DR SYGENE; SG10049; CBIQ.
KW COBALAMIN BIOSYNTHESIS; TRANSPORT; COBALT TRANSPORT; TRANSMEMBRANE.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 65 85 POTENTIAL.

```

```

FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
SQ SEQUENCE 225 AA; 25983 MW; E926FA4B CRC32;

Query Match 88.7%; Score 47; DB 2; Length 225;
Best Local Similarity 66.7%; Pred. No. 8.61e+00;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 202 rvlry 207
   1:||||
Qy 1 RILLY 6

RESULT 7
ID MMSA_PSEAE STANDARD; PRT; 496 AA.
AC P28810;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
DE (MMSDH).
GN MMSA.
OS PSEUDOMONAS AERUGINOSA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC PSEUDOMONADACEAE.
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 1-29.
RC STRAIN-PAO / ATCC 15692;
RX MEDLINE; 92317087.
RA STEELE M.I., LORENZ D., HATTER K., PARK A., SOKATCH J.R.;
RA J. BIOL. CHEM. 267:13585-13592(1992).
CC -!- CATALYTIC ACTIVITY: 2-METHYL-3-OXOPROPANATE + COA + NAD(+) -
CC PROPYL-COA + CO(2) + NADH.
CC -!- SUBUNIT: HOMODIMER.
CC -!- PATHWAY: DISTAL VALINE METABOLIC PATHWAY.
CC -!- INDUCTION: BY VALINE.
CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL; M84911; G151362; -.
DR PIR; B42902; B42902.
DR PIR; S27602; S27602.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU.
KW OXIDOREDUCTASE; NAD.
FT INIT_MET 0 0
FT ACT_SITE 281 281 BY SIMILARITY.
SQ SEQUENCE 496 AA; 53532 MW; 4D33C45B CRC32;

Query Match 88.7%; Score 47; DB 6; Length 496;
Best Local Similarity 66.7%; Pred. No. 8.61e+00;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 67 rvlry 72
   1:||||
Qy 1 RILLY 6

RESULT 8
ID HA1Q_MOUSE STANDARD; PRT; 328 AA.
AC P14428;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-Q ALPHA CHAIN (FRAGMENT).
GN H2-K.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85206119.
RA MORITA T., DELARBRE C., KRESS M., KOURILSKY P., GACHELIN G.;
RL IMMUNOGENETICS 21:367-383(1985).

```

CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 DR EMBL; M14827; G387471; -.
 DR HSSP; P01901; IYAA.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN.
 FT NON_TER 1
 FT DOMAIN <1 71
 FT DOMAIN 72 163
 FT DOMAIN 164 255
 FT DOMAIN 256 265
 FT DOMAIN 266 289
 FT TRANSMEM 289
 FT DOMAIN 290 328
 FT CYTOPLASMIC TAIL.
 FT DISULFID 82 145
 FT DISULFID 184 240
 FT CARBOHYD 67 67
 FT CARBOHYD 157 157
 FT CARBOHYD 157 157
 SQ SEQUENCE 328 AA; 36855 MW; 3845B867 CRC32;

Query Match 86.8%; Score 46; DB 4; Length 328;

Best Local Similarity 83.3%; Pred. No. 1.39e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 60 rllly 65

QY 1 RILLY 6

RESULT 9
 ID 1B20_HUMAN STANDARD; PRT; 338 AA.
 AC P30467;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2707 ALPHA CHAIN
 DE (B27-HS).
 GN HLAB.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91268545.
 RA CHOO Y.S., FAN L.A., HANSEN J.A.;
 RL J. IMMUNOL. 147:174-180(1991).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 DR EMBL; M62852; G187761; -.
 DR HSSP; P03989; ILSA.
 DR MIM; 142830; -.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN.
 FT DOMAIN 1 90
 FT DOMAIN 91 182
 FT DOMAIN 183 274
 FT DOMAIN 275 284
 FT TRANSMEM 285 308
 FT TRANSMEM 309 338
 FT CYTOPLASMIC TAIL.
 FT CARBOHYD 86 86
 FT DISULFID 101 164
 FT DISULFID 203 259
 FT DISULFID 203 259
 SQ SEQUENCE 338 AA; 37804 MW; 33FB8134 CRC32;

Query Match 86.8%; Score 46; DB 1; Length 338;

Best Local Similarity 83.3%; Pred. No. 1.39e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 rllly 84

QY 1 RILLY 6

QY 1 RILLY 6
 RESULT 10
 ID PPI2_TRYBB STANDARD; PRT; 346 AA.
 AC P23734;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE SERINE/THREONINE PROTEIN PHOSPHATASE PPI(5.9) (EC 3.1.3.16).
 OS TRYPAPOSOMA BRUCEI BRUCEI.
 OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; KINETOPLASTIDA;
 CC TRYPAPOSOMATIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90384806.
 RA EVERS R., CORNELISSEN A.W.C.A.;
 RL NUCLEIC ACIDS RES. 18:5089-5095(1990).
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O -> A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- TRYPAPOSOMA BRUCEI CONTAINS TWO PPI GENES WHICH ARE HIGHLY
 CC SIMILAR.
 CC -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-1
 CC SUBFAMILY.
 DR EMBL; X52746; G10509; -.
 DR PROSITE; PS00125; SER_THR_PHOSPHATASE.
 KW HYDROLASE; IRON; MANGANESE; MULTIGENE FAMILY.
 FT METAL 102 102
 FT METAL 104 104
 FT METAL 130 130
 FT METAL 162 162
 FT ACT_SITE 163 163
 FT METAL 211 211
 FT METAL 287 287
 SQ SEQUENCE 346 AA; 39294 MW; 0276BED5 CRC32;

Query Match 86.8%; Score 46; DB 7; Length 346;

Best Local Similarity 83.3%; Pred. No. 1.39e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 339 rllly 344

QY 1 RILLY 6

RESULT 11
 ID 1B14_HUMAN STANDARD; PRT; 361 AA.
 AC P03989;
 DT 23-OCT-1986 (REL. 02, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.
 GN HLAB.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86138405.
 RA WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;
 RL IMMUNOBIOLOGY 170:367-380(1985).
 RN [2]
 RP SEQUENCE OF 25-361 FROM N.A.
 RX MEDLINE; 86149317.
 RA SZOETS H., RIETHMUELLER G., WEISS E., MEO T.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 83:1428-1432(1986).
 RN [3]
 RP SEQUENCE OF 25-295.
 RX MEDLINE; 85226361.
 RA EZQUEIRA A., BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,
 RA LOPEZ DE CASTRO J.A.;
 RL BIOCHEMISTRY 24:1733-1741(1985).
 RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
 RX MEDLINE; 92405152.
 RA MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
 RL CELL 70:1035-1048(1992).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE; 92018187.
 RA MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
 RL NATURE 353:321-325(1991).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC -!- DISEASE: THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF
 CC ANKYLOSING SPONDYLITIS.
 DR EMBL; X03945; G32177; ALT_TERM.
 DR PIR; A25128; HLH02.
 DR PIR; S07441; S07441.
 DR PDB; 1HSA; 15-OCT-92.
 DR MIM; 142830; -.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 25 361 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN B-27.
 FT DOMAIN 25 114
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 309 332 CONNECTING PEPTIDE.
 FT DOMAIN 333 361 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CONFLICT 206 206
 FT CONFLICT 266 266
 FT STRAND 27 38
 FT TURN 39 41
 FT STRAND 42 52
 FT TURN 53 54
 FT STRAND 55 61
 FT TURN 62 63
 FT STRAND 70 71
 FT HELIX 74 76
 FT TURN 77 78
 FT HELIX 81 108
 FT TURN 109 110
 FT TURN 113 114
 FT STRAND 118 127
 FT TURN 129 130
 FT STRAND 133 142
 FT TURN 143 144
 FT STRAND 145 150
 FT TURN 152 153
 FT STRAND 157 159
 FT HELIX 162 173
 FT TURN 174 175
 FT HELIX 176 185
 FT TURN 186 186
 FT HELIX 187 198
 FT TURN 199 199
 FT HELIX 200 203
 FT TURN 204 204
 FT STRAND 207 207
 FT STRAND 210 217
 FT STRAND 222 233
 FT STRAND 238 243
 FT TURN 244 245
 FT STRAND 246 247
 FT HELIX 249 251
 FT STRAND 253 254
 FT STRAND 258 259
 FT STRAND 265 274

FT TURN 275 276
 FT HELIX 278 280
 FT STRAND 281 286
 FT TURN 288 289
 FT STRAND 294 296
 SQ SEQUENCE 361 AA; 40464 MW; 802130D5 CRC32;
 Query Match 86.8%; Score 46; DB 1; Length 361;
 Best Local Similarity 83.3%; Pred. No. 1.39e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 103 rllly 108
 QY 1 RLLRY 6
 RESULT 12
 ID HAL3_MOUSE STANDARD; PRT; 362 AA.
 AC P14426;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-K ALPHA CHAIN PRECURSOR.
 GN H2-D.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H;
 RX MEDLINE; 88060499.
 RA WATTS S., VOGEL J.M., HARRIMAN W.D., ITOH T., STAUSS H.J.,
 RA GOODENOW R.S.;
 RL J. IMMUNOL. 139:3878-3885(1987).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC EMBL; M18524; G387453; -.
 DR HSP; P01901; 1VAA.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 362 H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT D-K ALPHA CHAIN.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 307 333 CONNECTING PEPTIDE.
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110 POTENTIAL.
 FT CARBOHYD 200 200 POTENTIAL.
 FT CARBOHYD 280 280 POTENTIAL.
 SQ SEQUENCE 362 AA; 40620 MW; 7A34877E CRC32;
 Query Match 86.8%; Score 46; DB 4; Length 362;
 Best Local Similarity 83.3%; Pred. No. 1.39e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 103 rllly 108
 QY 1 RLLRY 6
 RESULT 13
 ID 1B18_HUMAN STANDARD; PRT; 362 AA.
 AC P10318;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2705 ALPHA CHAIN
DE PRECURSOR (B-27w) (B27.1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86220133.
RA SEMMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
RL EMBO J. 5:547-552(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86138405.
RA WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;
RL IMMUNOBIOLOGY 170:367-380(1985).
RN [3]
RP 3D-STRUCTURE MODELLING OF 115-206.
RA ROGNAN D., SCAPOZZA L., FOLKERS G., DASER A.;
RL SUBMITTED (JUL-1994) TO THE PDB DATA BANK.
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; X03665; G871297;
DR EMBL; X03666; G871297; JOINED.
DR EMBL; M12967; G187660;
DR PIR; A25092; HLHUBW.
DR PDB; 1ROG; 30-SEP-94.
DR PDB; 1ROH; 30-SEP-94.
DR PDB; 1ROI; 30-SEP-94.
DR PDB; 1ROJ; 30-SEP-94.
DR PDB; 1ROK; 30-SEP-94.
DR PDB; 1ROL; 30-SEP-94.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-27 B*2705.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40428 MW; 73243566 CRC32;
Query Match 86.8%; Score 46; DB 1; Length 362;
Best Local Similarity 83.3%; Pred. No. 1.39e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 103 rtfly 108
QY 1 RILLY 6
RESULT 14
ID 1B45_HUMAN STANDARD; PRT; 362 AA.
AC P30485;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-47 B*4701 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88227491.
RA CHOO S.Y., ST JOHN T., ORR H.T., HANSEN J.A.;
RL HUM. IMMUNOL. 21:209-219(1988).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; M54883; G187664;
DR HSSP; P03989; LHSA.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-27 B*2703.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.

RP SEQUENCE FROM N.A.
RX MEDLINE; 88152906.
RA ZEMMOUR J., ENNIS P.D., PARHAM P., DUPONT B.;
RL IMMUNOGENETICS 27:281-287(1988).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; M19756; G386776;
DR HSSP; P03989; LHSA.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN BW-47 B*4701.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 310 333 CONNECTING PEPTIDE.
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40571 MW; 67734C1E CRC32;
Query Match 86.8%; Score 46; DB 1; Length 362;
Best Local Similarity 83.3%; Pred. No. 1.39e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 103 rtfly 108
QY 1 RILLY 6
RESULT 15
ID 1B16_HUMAN STANDARD; PRT; 362 AA.
AC P19373;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2703 ALPHA CHAIN
DE PRECURSOR (B-27D).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88227491.
RA CHOO S.Y., ST JOHN T., ORR H.T., HANSEN J.A.;
RL HUM. IMMUNOL. 21:209-219(1988).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; M54883; G187664;
DR HSSP; P03989; LHSA.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-27 B*2703.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.

FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40402 MW; 7261C3AB CRC32;
Query Match 86.8%; Score 46; DB 1; Length 362;
Best Local Similarity 83.3%; Pred. No. 1.39e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 103 rllry 108
QY 1 RLLRY 6

Search completed: Thu May 22 08:28:09 1997
Job time : 11 secs.

THIS PAGE BLANK (USPTO)

PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 16; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.15e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIR 6
 ||| ||
 QY 1 YRLAIR 6

RESULT 9
 ID R92911 standard; peptide; 20 AA.
 AC R92911;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75/84-75).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*5-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 16; Length 20;
 Best Local Similarity 83.3%; Pred. No. 2.15e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIR 6
 ||| ||
 QY 1 YRLAIR 6

Search completed: Thu May 22 08:45:21 1997
 Job time : 10 secs.

DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702-60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 18; Length 20;

Best Local Similarity 83.3%; Pred. No. 2.15e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlair 6
 ||| ||
 QY 1 YRLAIR 6

RESULT

ID R95430 standard; peptide: 20 AA.

AC R95430;

DT 12-NOV-1996 (first entry)

DE HLA-B2702 84-75/75-84T palindrome.

KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;

KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;

KW cytotoxic; antigen presenting cell.

OS Synthetic.

PN W09513298-A1.

PD 18-MAY-1995.

PF 10-NOV-1994; U12985.

PR 10-NOV-1993; US-150493.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM;

DR WPI; 95-194027/25.

PT Compens. comprising lymphoid surface membrane proteins - which may

PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 12; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of

CC HLA-B2702 84-75/75-84T palindrome. These sequences can be used to

CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface

CC membrane protein associated with T-cell activation in mammalian T-cells,

CC and is also immunologically cross reactive with the heat shock protein

CC Hsc70. p74 is found in a limited number of cell types, but is

CC particularly expressed on B and T cells. p74 can be isolated by lysis of

CC a suitable cell with an amphoteric detergent, and then passed through an

CC affinity column containing a covalently bound HLA-B2702 palindromic

CC peptide. Compositions comprising the extracellular fragment of p74

CC combined with HLA-B2702-60-84 (see R95416), induces calcium influx, and

CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.

CC Candidate compounds can be screened for their effect on the cytolytic

CC activity of T-cells, by combining them with the extracellular portion of

CC p74 and determining the amount of binding between the candidate compound

CC and p74. Modulation of CTL activity can be inhibited in a cellular

CC composition containing T-cells and antigen presenting cells (APCs), by

CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 18; Length 20;

Best Local Similarity 83.3%; Pred. No. 2.15e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlair 6
 ||| ||
 QY 1 YRLAIR 6

RESULT

ID R92907 standard; peptide: 20 AA.

AC R92907;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class

CC I MHC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 16; Length 20;

Best Local Similarity 83.3%; Pred. No. 2.15e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlair 6
 ||| ||
 QY 1 YRLAIR 6

RESULT

ID R92909 standard; peptide: 20 AA.

AC R92909;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PA (DOHE-) DOHENY EYE INST.
 PI Suzuki S;
 DR WPI; 96-068873/07.
 DR N-PSDB; T03617.
 PT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat
 pc5 - involved in cell-cell adhesion and regulation activities
 PS Example 2; Page 67-68; 146pp; English.
 CC R87142-R87144 represent partial fragments of the drosophila protocadherin
 CC sequence. The cDNAs encoding these sequences were isolated after
 CC screening a drosophila whole body cDNA preparation with the primers shown
 CC in R03575 and T03576. The primers were constructed from portions of the
 CC amino acid sequences of the third and fourth extracellular domains of
 CC published cadherin sequences. The cytoplasmic domain of cadherin
 CC interacts with the cytoskeleton through catenins and other cytoskeleton
 CC associated proteins. The cytoplasmic domain is not present in all
 CC cadherins, but in those which possess it, it is essential for the
 CC cadherins adhesive function. The cadherins which do not possess a
 CC cytoplasmic domain appear to function via a different method from those
 CC with a cytoplasmic domain. These protein sequences are involved in
 CC cell-cell adhesion. These sequences may have regulatory functions in the
 CC cell, as well as the cell-cell adhesive properties. Antibodies produced
 CC against these sequences are useful for modulating the binding activity of
 CC these protocadherins, and can be used therapeutically.
 SQ Sequence 43 AA;

Query Match 86.8%; Score 46; DB 17; Length 43;
 Best Local Similarity 83.3%; Pred. No. 7.66e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 YRLVIR 16
 |||||
 QY 1 YRLLIIR 6

RESULT 3
 ID R61548 standard; peptide; 10 AA.
 AC R61548;
 DE Peptide fragment (1.0914) of HPV binds HLA-A2.1.
 DT HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW antigen; epitope; immunoregulatory target protein; PSA; HBVC; HBVs; EBV;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; Smer; 10mer; anchor; human leukocyte antigen.
 OS Human papilloma virus strain 18.
 PN WO9420127-A.
 PD 15-SEP-1994.
 PF 04-MAR-1994; U02353.
 PR 05-MAR-1993; US-027146.
 PR 04-JUN-1993; US-073205.
 PR 29-NOV-1993; US-159184.
 PA (CYTE-) CYTEL CORP.
 PI Grey HM, Kast WM, Sette A, Sidney J;
 DR WPI; 94-302678/37.
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.

PS Example 5; Page 109; 138pp; English.
 CC R59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1
 CC binding motif. These peptides bind HLA-A2.1 and have a binding
 CC affinity of at least 1% as compared to a reference peptide (R71293).
 CC R61548 has an IC50 of 0.0036 and the sequence occurs at position 24
 CC in the HPV E6 protein. The peptides of the invention can induce
 CC cytotoxic T lymphocytes which can react with target cells. They can
 CC be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 SQ Sequence 10 AA;

Query Match 81.1%; Score 43; DB 11; Length 10;
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

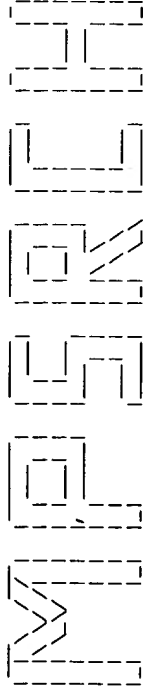
Db 3 YNLIIR 8
 |||||
 QY 1 YRLLIIR 6

RESULT 4
 ID R95429 standard; peptide; 12 AA.
 AC R95429;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-79-84 palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-79-84 palindromic. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 12 AA;

Query Match 79.2%; Score 42; DB 18; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2.15e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIR 6
 |||||
 QY 1 YRLLIIR 6

RESULT 5
 ID R95428 standard; peptide; 20 AA.
 AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75-84 palindromic.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:45:11 1997; MasPar time 1.73 seconds
Tabular output not generated. 37.783 Million cell updates/sec

Title: >US-08-653-294-6
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 YRLLR 6

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 16.490; Variance 45.535; scale 0.362

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------------------------|-----------|
| 1 | 46 | 86.8 | 43 | 11 | R58902 Drosophila-12 cadher | 7.66e+01 |
| 2 | 46 | 86.8 | 43 | 17 | R87142 Protocadherin clone D | 7.66e+01 |
| 3 | 43 | 81.1 | 10 | 11 | R61548 Peptide fragment (1-10 | 1.66e+02 |
| 4 | 42 | 79.2 | 12 | 18 | R35429 HLA-B*2702 84-79-84 pa | 2.15e+02 |
| 5 | 42 | 79.2 | 20 | 18 | R95428 HLA-B*2702 84-75-84 pa | 2.15e+02 |
| 6 | 42 | 79.2 | 20 | 18 | R95430 HLA-B*2702 84-75T/75-8 | 2.15e+02 |
| 7 | 42 | 79.2 | 20 | 16 | R92907 HLA-B*2702 CTL modul | 2.15e+02 |
| 8 | 42 | 79.2 | 20 | 16 | R92909 HLA-B*2702 CTL modul | 2.15e+02 |
| 9 | 42 | 79.2 | 20 | 16 | R92911 HLA-B*2702 CTL modul | 2.15e+02 |

Note: Post-processor removed 36 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID R58902 standard; Protein; 43 AA.
AC R58902;
DT 17-APR-1995 (first entry)

DE Drosophila-12 cadherin-related molecule.
KW Cadherin; cell adhesion molecule.
OS Drosophila.
PN WO9414960-A.
PD 07-JUL-1994.
PF 23-DEC-1993; U12588.
PR 29-DEC-1992; US-998003.
PA (DOHE-) DOHENY EYE INST.
PI Suzuki S.
DR WPI; 94-293849/36.
DR N-PSDB; Q68993.
PT Polynucleotide sequences encoding new proto:cadherins - useful
PT for modulating natural binding and regulating activities.
PS Example; Page 63; 114pp; English.
CC Two regions of conserved AA sequence, one from the middle of the
CC third cadherin extracellular subdomain (EC-3) and the other from the
CC C-terminus of the fourth extracellular subdomain (EC-4) were
CC identified. The corresp. degenerate oligos (Q68949, Q68950) were
CC designed for use as PCR primers. PCR was carried out on a rat brain
CC cDNA prep. Two major bands of about 450 bps and 130 bps were found.
CC The 450 bp band corresponded to the expected length between the two
CC primer sites, but the 130 bp band could not be predicted from any
CC of the previously identified cadherin sequences. The 450 bp and 130
CC bp bands were extracted and sequenced. Nineteen novel partial cDNA
CC clones were isolated. The DNA and deduced AA sequences of the
CC clones (including sequences corresp. to the PCR primers) are given
CC in Q68951-Q68959 and R58860-R58878. Various cDNA fragments
CC structurally similar to the rat cDNAs were isolated from human,
CC C. elegans whole body cDNA preps, and from Drosophila and
CC mouse and Xenopus brain cDNA preps, by PCR using the above primers.
CC The DNA and deduced AA sequences of the resulting PCR fragments
CC (including sequences corresp. to the PCR primers) are given in
CC Q68971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison
CC of the deduced AA sequences indicates a similarity, in particular,
CC there are three sets of clones that appear to be cross-species
CC homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and
CC HUMAN-11; and MOUSE-326 and HUMAN-42.
SQ Sequence 43 AA;

Query Match 86.8%; Score 46; DB 11; Length 43;
Best Local Similarity 83.3%; Pred. No. 7.66e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 yrlvir 16
| | | | |
Qy 1 YRLLR 6

RESULT 2
ID R87142 standard; Peptide; 43 AA.
AC R87142;
DT 29-AUG-1996 (first entry)
DE Protocadherin clone DROSOPHILA-12.
KW Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse;
KW catenin; therapy; clone; frog; fruit fly.
OS Drosophila melanogaster.
FH Key Location/Qualifiers
FT Misc_difference 38
FT /note= "encoded by CGA"
FT /note= "encoded by 39
FT /note= "encoded by ATG"
FT Misc_difference 40
FT /note= "encoded by ACA"
FT /note= "encoded by 41
FT Misc_difference 41
FT /note= "encoded by ATG"
FT /note= "encoded by 42
FT Misc_difference 42
FT /note= "encoded by CGC"
FT /note= "encoded by 43
FT Misc_difference 43
FT /note= "encoded by CGC"
PN WO9600289-A1.
PD 04-JAN-1996.
PF 26-JUN-1995; U08071.
PR 27-JUN-1994; US-268161.

WISREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:26:43 1997; MasPar time 2.78 Seconds
Tabular output not generated. 61.517 Million cell updates/sec

Title: >US-08-653-294-4
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 RIALRY 6

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 21.604; Variance 27.804; scale 0.777

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------------------------------|-----------|
| 1 | 49 | 100.0 | 273 13 | I38509 MHC class I histocompat | 3.39e+00 |
| 2 | 49 | 100.0 | 274 2 | HLHU32 MHC class I histocom | 3.39e+00 |
| 3 | 49 | 100.0 | 274 13 | I54463 MHC HLA-B*38 chain - | 3.39e+00 |
| 4 | 49 | 100.0 | 354 13 | I59308 class I histocompat | 3.39e+00 |
| 5 | 49 | 100.0 | 354 13 | I80168 class I histocompat | 3.39e+00 |
| 6 | 49 | 100.0 | 354 13 | I80167 class I histocompat | 3.39e+00 |
| 7 | 49 | 100.0 | 355 13 | I80171 class I histocompat | 3.39e+00 |
| 8 | 49 | 100.0 | 355 13 | I80169 class I histocompat | 3.39e+00 |
| 9 | 49 | 100.0 | 359 2 | HLHU12 MHC class I histocom | 3.39e+00 |
| 10 | 49 | 100.0 | 362 13 | I62045 gene HLA B-1517 prot | 3.39e+00 |
| 11 | 49 | 100.0 | 362 13 | I59633 MHC HLA-B transmembr | 3.39e+00 |
| 12 | 49 | 100.0 | 362 13 | I37521 HLA-B*57.2 antigen - | 3.39e+00 |
| 13 | 49 | 100.0 | 362 13 | I84486 transmembrane glycop | 3.39e+00 |
| 14 | 49 | 100.0 | 362 13 | I84490 lymphocyte antigen - | 3.39e+00 |
| 15 | 49 | 100.0 | 362 6 | A45834 MHC class I histocom | 3.39e+00 |
| 16 | 49 | 100.0 | 362 2 | HLHUB8 MHC class I histocom | 3.39e+00 |
| 17 | 49 | 100.0 | 362 6 | B30345 MHC class I histocom | 3.39e+00 |
| 18 | 49 | 100.0 | 362 6 | JH0541 class I histocompat | 3.39e+00 |
| 19 | 49 | 100.0 | 362 6 | JH0540 class I histocompat | 3.39e+00 |
| 20 | 49 | 100.0 | 362 6 | A30345 MHC class I histocom | 3.39e+00 |
| 21 | 49 | 100.0 | 362 6 | S24434 class I histocompat | 3.39e+00 |

22 49 100.0 362 6 JH0539 class I histocompat 3.39e+00
23 49 100.0 362 13 I37120 MCH class I HLA-B*51 3.39e+00
24 49 100.0 363 16 S07113 class I histocompat 3.39e+00
25 49 100.0 363 13 I36957 MHC ChIA chain - chi 3.39e+00
26 49 100.0 363 6 S03537 class I histocompat 3.39e+00
27 49 100.0 364 6 D35997 MHC class I histocom 3.39e+00
28 49 100.0 364 6 A35997 MHC class I histocom 3.39e+00
29 49 100.0 365 13 I54493 HLA-A protein - huma 3.39e+00
30 49 100.0 365 6 JH0537 class I histocompat 3.39e+00
31 49 100.0 365 13 I54416 HLA-AW24 protein - h 3.39e+00
32 46 93.9 161 14 I48932 adenosine receptor s 1.34e+01
33 46 93.9 409 14 I48095 A2 adenosine recepto 1.34e+01
34 46 93.9 410 14 A48974 adenosine receptor A 1.34e+01
35 46 93.9 412 13 A48978 adenosine A2 recepto 1.34e+01
36 46 93.9 412 16 JG4844 adenosine receptor A 1.34e+01
37 46 93.9 412 13 S37160 adenosine receptor A 1.34e+01
38 46 93.9 412 13 D30341 G protein-coupled re 1.34e+01
39 46 93.9 505 16 S61307 membrane-bound nitr 1.34e+01
40 46 93.9 652 11 S52683 probable membrane pr 1.34e+01
41 46 93.9 1220 12 S64916 apolipoprotein(a) (E 1.34e+01
42 46 93.9 1420 5 A32869 COX10 protein precu 2.09e+01
43 45 91.8 482 2 C0B710 DNA-directed RNA pol 2.09e+01
44 45 91.8 880 5 S04717 pyrimidine synthesis 2.09e+01
45 45 91.8 2225 2 A23443

ALIGNMENTS

RESULT 1
ENTRY I38509 #type fragment
TITLE MHC class I histocompatibility antigen - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 06-Sep-1996
ACCESSIONS I38509
REFERENCE I38509
#authors Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
#journal Tissue Antigens (1994) 44:271-273
#title HLA-B*5105: a newly identified B51 IEF variant.
#cross-references MUID:95176331
#accession I38509
##status preliminary; translated from GB/EMBL/DBBJ
##molecule_type mRNA
##residues 1-273 ##label RES
#cross-references EMBL:U06697; NID:g469544; CDS_PID:g469545
GENETICS
#note gene name HLA-B
SUMMARY #length 273 #checksum 6533
Query Match 100.0%; Score 49; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 78 rialry 83
Qy 1 RIALRY 6
RESULT 2
ENTRY HLHU32 #type fragment
TITLE MHC class I histocompatibility antigen HLA-A32 alpha chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 06-Sep-1996
ACCESSIONS A26088
REFERENCE A26088
#authors Wan, A.M.; Ennis, P.; Parham, P.; Holmes, N.
#journal J. Immunol. (1986) 137:3671-3674
#title The primary structure of HLA-A32 suggests a region involved in formation of the Bw4/Bw6 epitopes.
#cross-references MUID:87058961
#accession A26088

```
##molecule_type protein
##residues 1-274 ##label WAN
GENETICS
#gene GDB:HLA-A
##cross-references GDB:l19310
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS glycoprotein; heterodimer; transmembrane protein;
transplantation antigen
FEATURE
196-261 #domain immunoglobulin homology #label IMM
SUMMARY
#length 274 #checksum 899
Query Match 100.0%; Score 49; DB 2: Length 274;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 79 r1aly 84
|||||
QY 1 RIALY 6
RESULT 3
ENTRY #type fragment
TITLE MHC HLA-B38 chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
07-Jun-1996
ACCESSIONS I54463
REFERENCE I54463
#authors Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.;
Weiss, E.; Schmidt, H.
#journal Immunogenetics (1989) 30:200-207
#title Genetic and serological heterogeneity of the supertypic HLA-B
locus specificities Bw4 and Bw6.
#cross-references MUID:89379286
#accession I54463
#status preliminary; translated from GB/EMBL/DBDJ
##molecule_type DNA
##residues 1-274 ##label RES
##cross-references GB:M29864; NID:g187674; CDS_PID:g187675
SUMMARY #length 274 #checksum 1031
Query Match 100.0%; Score 49; DB 13: Length 274;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 79 r1aly 84
|||||
QY 1 RIALY 6
RESULT 4
ENTRY #type fragment
TITLE class I histocompatibility antigen - pygmy chimpanzee
(fragment)
ORGANISM #formal_name Pan paniscus #common_name pygmy chimpanzee,
bonobo
DATE 31-May-1996 #sequence_revision 31-May-1996 #text_change
31-May-1996
ACCESSIONS I59308
REFERENCE I59308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I59308
#status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-354 ##label RES
##cross-references EMBL:U05575; NID:g454767; CDS_PID:g454768
SUMMARY #length 354 #checksum 3211
Query Match 100.0%; Score 49; DB 13: Length 354;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 95 r1aly 100
|||||
QY 1 RIALY 6
SUMMARY #length 354 #checksum 3211
Query Match 100.0%; Score 49; DB 13: Length 354;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 95 r1aly 100
|||||
QY 1 RIALY 6
RESULT 5
ENTRY #type fragment
TITLE class I histocompatibility antigen - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996
ACCESSIONS I80168
REFERENCE I59308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I80168
#status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-354 ##label RES
##cross-references EMBL:U05579; NID:g454775; CDS_PID:g454776
SUMMARY #length 354 #checksum 5067
Query Match 100.0%; Score 49; DB 13: Length 354;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 95 r1aly 100
|||||
QY 1 RIALY 6
RESULT 6
ENTRY #type fragment
TITLE class I histocompatibility antigen - pygmy chimpanzee
(fragment)
ORGANISM #formal_name Pan paniscus #common_name pygmy chimpanzee,
bonobo
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996
ACCESSIONS I80167
REFERENCE I59308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I80167
#status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-354 ##label RES
##cross-references EMBL:U05578; NID:g454773; CDS_PID:g454774
SUMMARY #length 354 #checksum 3983
Query Match 100.0%; Score 49; DB 13: Length 354;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 95 r1aly 100
|||||
QY 1 RIALY 6
RESULT 7
ENTRY #type fragment
```

```

TITLE      class I histocompatibility antigen - chimpanzee (fragment)
ORGANISM   #formal_name Pan troglodytes #common_name chimpanzee
DATE       24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996

ACCESSIONS I80171
REFERENCE   159308
AUTHORS    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
            A.L.; Bontrop, R.E.; Watkins, D.I.
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
TITLE      A uniquely high level of recombination at the HLA-B locus.
CROSS-REFERENCES MUID:94286544
ACCESSION  I80171
STATUS     preliminary; translated from GB/EMBL/DBDJ
MOLECULE   1-355 #label RES
RESIDUES   #cross-references EMBL:U05582; NID:9454781; CDS_PID:9454782
SUMMARY    #length 355 #checksum 6021

Query Match      100.0%; Score 49; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 rialry 100
      |||||
QY 1 RIALRY 6

RESULT 8
ENTRY   class I histocompatibility antigen - chimpanzee (fragment)
TITLE   #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE     24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996

ACCESSIONS I80169
REFERENCE   159308
AUTHORS    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
            A.L.; Bontrop, R.E.; Watkins, D.I.
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
TITLE      A uniquely high level of recombination at the HLA-B locus.
CROSS-REFERENCES MUID:94286544
ACCESSION  I80169
STATUS     preliminary; translated from GB/EMBL/DBDJ
MOLECULE   1-355 #label RES
RESIDUES   #cross-references EMBL:U05580; NID:9454777; CDS_PID:9454778
SUMMARY    #length 355 #checksum 4603

Query Match      100.0%; Score 49; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 rialry 100
      |||||
QY 1 RIALRY 6

RESULT 9
ENTRY   HLH12
TITLE   MHC class I histocompatibility antigen HLA alpha chain
ORGANISM #formal_name Homo sapiens #common_name human
DATE     05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change
15-Jun-1996

ACCESSIONS A02189
REFERENCE   A02189
AUTHORS    Malissen, M.; Malissen, B.; Jordan, B.R.
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
TITLE      Exon/intron organization and complete nucleotide sequence of
            an HLA gene.
CROSS-REFERENCES MUID:82151002
ACCESSION  A02189
MOLECULE   1-359 #label MAL
RESIDUES

```

```

COMMENT      The seven exons correspond approximately to the domain structure of
              this chain.

GENETICS     #map-position 6p21.3
              #introns 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
              immunoglobulin homology
KEYWORDS     duplication; glycoprotein; heterodimer; transmembrane
              protein; transplantation antigen
FEATURE      #domain signal sequence #status predicted #label SIG\
              #product class I histocompatibility antigen HLA alpha
              chain #status predicted #label MAT\
              #domain alpha-1 #label EX1\
              #domain alpha-2 #label EX2\
              #domain immunoglobulin homology #label IMM\
              #domain transmembrane #status predicted #label TMM\
              #domain intracellular #status predicted #label INT\
              #binding site carbohydrate (Asn) (covalent) #status
              predicted\
              #disulfide_bonds #status predicted
              #length 359 #molecular_weight 40548 #checksum 2195
SUMMARY

Query Match      100.0%; Score 49; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 100 rialry 105
      |||||
QY 1 RIALRY 6

RESULT 10
ENTRY   I62045
TITLE   gene HLA B-1517 protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
13-Sep-1996

ACCESSIONS I62045
REFERENCE   I38421
AUTHORS    Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
            Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
            Bias, W.B.; Parham, P.
JOURNAL    Tissue Antigens (1994) 43:209-218
TITLE      HLA-B*51: a widespread and diverse family of HLA-B alleles.
CROSS-REFERENCES MUID:94367483
ACCESSION  I62045
STATUS     preliminary; translated from GB/EMBL/DBDJ
MOLECULE   1-362 #label RES
RESIDUES   #cross-references EMBL:U01848; NID:9402676; CDS_PID:9402677
GENETICS
NOTE       gene name HLA B-1517
SUMMARY    #length 362 #molecular_weight 40417 #checksum 7730

Query Match      100.0%; Score 49; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
      |||||
QY 1 RIALRY 6

RESULT 11
ENTRY   I59633
TITLE   MHC HLA-B transmembrane glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996

ACCESSIONS I59633
REFERENCE   I59633

```

```

#authors      Hildebrand, W.H.; Domena, J.D.; Parham, P.
#journal      Tissue Antigens (1993) 41:190-195
#title        Primary structure shows HLA-B59 to be a hybrid of HLA-B55 and
              HLA-B51, and not a subtype of HLA-B8.
#cross-references MIM:193369833
#accession    159633
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-362 ##label RES
#cross-references GB:L07743; NID:g388314; CDS_PID:g388315

GENETICS
#note
#summary      gene name HLA-B
              #length 362 #molecular-weight 40584 #checksum 8821

Query Match 100.0%; Score 49; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
   |||||
Qy 1 RIALRY 6

RESULT 12
ENTRY
TITLE      HLA-Bw57.2 antigen - human
#formal_name Homo sapiens #common_name man
ORGANISM
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
          02-Jul-1996

ACCESSIONS
REFERENCE  I37521
#authors   Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,
              R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
              Pezli-Ertler, M.L.; Du Toit, E.D.; Parham, P.
#journal   J. Immunol. (1992) 149:3411-3415
#title     Distinctive HLA-A,B antigens of black populations formed by
              interallelic conversion.
#cross-references MIM:93056508
#accession I37521
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues   1-362 ##label RES
#cross-references EMBL:X61707; NID:g32186; CDS_PID:g32187
              #length 362 #molecular-weight 40342 #checksum 7369

SUMMARY
Query Match 100.0%; Score 49; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
   |||||
Qy 1 RIALRY 6

RESULT 13
ENTRY
TITLE      transmembrane glycoprotein - human
#formal_name Homo sapiens #common_name man
ORGANISM
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
          02-Aug-1996

ACCESSIONS
REFERENCE  I84486
#authors   Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
              Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
              Blas, W.B.; Parham, P.
#journal   Tissue Antigens (1994) 43:209-218
#title     HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MIM:94367483
#accession I84486
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues   1-362 ##label RES
#cross-references GB:L15005; NID:g493154; CDS_PID:g493155

```

```

GENETICS
#note
#summary      gene name HLA-B*1513
              #length 362 #molecular-weight 40378 #checksum 9453

Query Match 100.0%; Score 49; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
   |||||
Qy 1 RIALRY 6

RESULT 14
ENTRY
TITLE      lymphocyte antigen - human
#formal_name Homo sapiens #common_name man
ORGANISM
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
          02-Aug-1996

ACCESSIONS
REFERENCE  I84490
              I38518
#authors   Browning, M.J.; Madrigal, J.A.; Krausa, P.; Kowalski, H.;
              Allsopp, C.E.; Little, A.M.; Turner, S.; Adams, E.J.;
              Arnett, K.L.; Bodmer, W.F.; Bodmer, J.G.; Parham, P.
#journal   Tissue Antigens (1995) 45:177-187
#title     The HLA-A,B,C genotype of the class I negative cell line
              Daudi reveals novel HLA-A and -B alleles.
#cross-references MIM:95282145
#accession I84490
              #status     preliminary; translated from GB/EMBL/DBJ
              #molecule_type mRNA
              #residues   1-362 ##label RES
              #cross-references GB:L33923; NID:g520836; CDS_PID:g520837

GENETICS
#note
#summary      gene name HLA-A10-B38
              #length 362 #molecular-weight 40355 #checksum 8277

Query Match 100.0%; Score 49; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
   |||||
Qy 1 RIALRY 6

RESULT 15
ENTRY
TITLE      MHC class I histocompatibility antigen HLA-B53 alpha chain
              precursor - human
#formal_name Homo sapiens #common_name man
ORGANISM
DATE       03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change
          06-Sep-1996

ACCESSIONS
REFERENCE  A45834
              A45834
#authors   Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.;
              Takiguchi, M.
#journal   Immunogenetics (1990) 32:195-199
#title     Allotopespecificities between HLA-Bw53 and HLA-B35 are generated
              by substitution of the residues associated with HLA-Bw4/Bw6
              public epitopes.
#accession A45834
#molecule_type DNA
#residues   1-362 ##label HAY
#cross-references GB:M58636; GB:M33574
#note       this allele is designated B*5301

GENETICS
#gene       GDB:HLA-B
#cross-references GDB:120048
#map_position gp21.3-6p21.3
CLASSIFICATION
#classification Immunoglobulin homology
KEYWORDS
#keywords     heterodimer; transmembrane protein

```

```

FEATURE
1-24      #domain signal sequence #status predicted #label SIG\
220-285   #domain immunoglobulin homology #label IMM\
110       #binding_site carbohydrate (Asn) (covalent) #status
          predicted
SUMMARY   #length 362 #molecular-weight 40495 #checksum 9558

Query Match      100.0%; Score 49; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
   |||||
QY 1 RIALRY 6

```

Search completed: Thu May 22 08:27:07 1997
Job time : 24 secs.

THIS PAGE BLANK (USPTO)

 M I S R E H

 (TM)

 Release 2.1D John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
 Distribution rights by Inteligenetics, Inc.

MPSrch.pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu May 22 08:27:25 1997; MasPar time 1.93 Seconds
 Tabular output not generated. 33.906 Million cell updates/sec

Title: >US-08-653-294-4
 Description: (1-6) from US08653294.pep
 Perfect Score: 49
 Sequence: 1 RIALRY 6

Scoring table: PAM 150
 Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq26
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19

Statistics: Mean 15.638; Variance 39.027; scale 0.401

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description | Pred. No. |
|------------|-------|---------------|--------|--------|-----------------------|-----------|
| 1 | 49 | 100.0 | 10 18 | R95413 | Alphal-helix of HLA-B | 1.25e+01 |
| 2 | 49 | 100.0 | 10 18 | R95425 | HLA-B2702.75-84(D) | 1.25e+01 |
| 3 | 49 | 100.0 | 10 8 | R41208 | Peptide fragment of C | 1.25e+01 |
| 4 | 49 | 100.0 | 10 16 | R33062 | HLA-B2702 CTL modul | 1.25e+01 |
| 5 | 49 | 100.0 | 10 16 | R33094 | HLA-B2702 CTL modul | 1.25e+01 |
| 6 | 49 | 100.0 | 12 18 | R95429 | HLA-B2702 84-79-84 pa | 1.25e+01 |
| 7 | 49 | 100.0 | 15 16 | R32912 | HLA-B2702 CTL modul | 1.25e+01 |
| 8 | 49 | 100.0 | 20 18 | R95428 | HLA-B2702 84-75-84 pa | 1.25e+01 |
| 9 | 49 | 100.0 | 20 16 | R32907 | HLA-B2702 CTL modul | 1.25e+01 |
| 10 | 49 | 100.0 | 20 16 | R32908 | HLA-B2702 CTL modul | 1.25e+01 |
| 11 | 49 | 100.0 | 25 18 | R95416 | HLA-B2702.60-84. | 1.25e+01 |
| 12 | 49 | 100.0 | 25 18 | R95422 | HLA-B38.6084 | 1.25e+01 |
| 13 | 49 | 100.0 | 25 16 | R33090 | HLA-B2702 CTL modul | 1.25e+01 |
| 14 | 49 | 100.0 | 25 8 | R41205 | Peptide fragment of C | 1.25e+01 |
| 15 | 49 | 100.0 | 25 16 | R33093 | HLA-B38 CTL modul | 1.25e+01 |
| 16 | 49 | 100.0 | 25 8 | R48286 | Peptide fragment of H | 1.25e+01 |
| 17 | 49 | 100.0 | 362 3 | R12463 | HLA-Bw53 exon. | 1.25e+01 |
| 18 | 49 | 100.0 | 362 2 | R03142 | Sequence of HLA-Bw52 | 1.25e+01 |
| 19 | 49 | 100.0 | 362 2 | R03144 | Sequence of HLA-B51 a | 1.25e+01 |
| 20 | 47 | 95.9 | 939 1 | R04104 | pJH1 gene product - b | 2.26e+01 |

| | | | | | | |
|----|----|------|--------|--------|-----------------------|----------|
| 21 | 46 | 93.9 | 349 19 | W02658 | G-protein coupled dog | 3.03e+01 |
| 22 | 46 | 93.9 | 349 16 | R48686 | G-protein coupled dog | 3.03e+01 |
| 23 | 46 | 93.9 | 412 9 | R47387 | Human A2a adenosine r | 3.03e+01 |
| 24 | 46 | 93.9 | 412 15 | R84193 | Human A2a adenosine r | 3.03e+01 |
| 25 | 46 | 93.9 | 412 18 | R33990 | Human ventricle A2a a | 3.03e+01 |
| 26 | 46 | 93.9 | 412 8 | R41525 | Human A2a adenosine r | 3.03e+01 |
| 27 | 46 | 93.9 | 412 16 | R87656 | Human adenosine recep | 3.03e+01 |
| 28 | 45 | 91.8 | 43 18 | R92804 | PB145 serpin enzyme c | 4.07e+01 |
| 29 | 45 | 91.8 | 959 14 | R76066 | Yeast MSH1 protein. | 4.07e+01 |
| 30 | 45 | 91.8 | 971 14 | R76070 | Yeast MSH1 protein.wi | 4.07e+01 |
| 31 | 42 | 85.7 | 10 18 | R95426 | HLA-B2702.75-84(I) | 9.64e+01 |
| 32 | 42 | 85.7 | 10 16 | R83096 | HLA-B2702 CTL modul | 9.64e+01 |
| 33 | 42 | 85.7 | 10 16 | R83095 | HLA-B2702 CTL modul | 9.64e+01 |
| 34 | 42 | 85.7 | 20 16 | R92910 | HLA-B2702 CTL modul | 9.64e+01 |
| 35 | 42 | 85.7 | 20 16 | R92909 | HLA-B2702 CTL modul | 9.64e+01 |
| 36 | 42 | 85.7 | 1165 7 | R37309 | Cardiac adenylyl cycl | 9.64e+01 |
| 37 | 42 | 85.7 | 3567 8 | R44431 | eryA region polypepti | 9.64e+01 |
| 38 | 41 | 83.7 | 314 19 | W02659 | G-protein coupled dog | 1.28e+02 |
| 39 | 41 | 83.7 | 326 9 | R45744 | Human A1 adenosine re | 1.28e+02 |
| 40 | 41 | 83.7 | 326 8 | R41524 | Human A1 adenosine re | 1.28e+02 |
| 41 | 41 | 83.7 | 326 9 | R47386 | Human A1 adenosine re | 1.28e+02 |
| 42 | 41 | 83.7 | 326 4 | R22007 | A1 adenosine receptor | 1.28e+02 |
| 43 | 41 | 83.7 | 326 18 | R93989 | Human ventricle A1 ad | 1.28e+02 |
| 44 | 41 | 83.7 | 335 1 | P80386 | DNA polymerase beta 1 | 1.28e+02 |
| 45 | 41 | 83.7 | 593 5 | R05874 | Hsp70 antigen of Myco | 1.28e+02 |

ALIGNMENTS

RESULT 1
 ID R95413 standard; peptide; 10 AA.

AC R95413;
 DT 12-NOV-1996 (first entry)
 DE Alphal-helix of HLA-B2702
 KW HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 PS This sequence represents the alphal-helix of the
 CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10
 | | | | |
 QY 1 RIALRY 6

RESULT 2

ID R95425 standard; peptide; 10 AA.
 AC R95425;
 DT 12-NOV-1996 (first entry)
 DE HLA-B*2702.75-84(D).
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc difference 3
 FT /note= "N3D mutation"
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*2702.75-84(D). These sequences can be used to isolate the protein
 CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B*2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10
 | | | | |
 QY 1 RIALRY 6

RESULT 3

ID R41208 standard; peptide; 10 AA.
 AC R41208;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN W09317699-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI; 93-303134/38.
 PT New peptides(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 11; Page 54; 61pp; English.
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
 CC activity, either by inhibition or stimulation. It can be used
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 CC This peptide sequence is more commonly found within larger peptide
 CC compounds of not more than 30 amino acids in length.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10
 | | | | |
 QY 1 RIALRY 6

RESULT 4

ID R83062 standard; peptide; 10 AA.
 AC R83062;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW Class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358382/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Claim 15; Page 9; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R82907-R82913 represent fragments of
 CC Class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10
 | | | | |
 QY 1 RIALRY 6

RESULT 5

ID R83094 standard; peptide; 10 AA.
 AC R83094;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.75-84(D)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 14; Page 34; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with
 CC a subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 10 AA;

 Query Match 100.0%; Score 49; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Db 5 rialry 10
 | | | | |
 Qy 1 RIALRY 6

 RESULT 6
 ID R95429 standard; peptide; 12 AA.
 AC R95429;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-79-84 palindromic.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702 60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 12 AA;

 Query Match 100.0%; Score 49; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Db 7 rialry 12
 | | | | |
 Qy 1 RIALRY 6

 RESULT 7
 ID R92912 standard; peptide; 15 AA.
 AC R92912;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.70-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 15 AA;

 Query Match 100.0%; Score 49; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Db 10 rialry 15
 | | | | |
 Qy 1 RIALRY 6

 RESULT 8
 ID R95428 standard; peptide; 20 AA.
 AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75-84 palindromic.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.

PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75-84 palindromic. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxic. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 r1aly 20
 |||||
 QY 1 RIALRY 6

RESULT 9

ID R92907 standard; peptide; 20 AA.
 AC R92907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 r1aly 20
 |||||

QY 1 RIALRY 6
 RESULT 10
 ID R92908 standard; peptide; 20 AA.
 AC R92908;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 r1aly 20
 |||||
 QY 1 RIALRY 6

RESULT 11

ID R95416 standard; peptide; 25 AA.
 AC R95416;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702.60-84.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytotoxic; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents
 CC HLA-B2702.60-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an

CC amphoteretic detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC this sequence, induces calcium influx, and inhibits cytotoxic T
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can
 CC be screened for their effect on the cytolytic activity of T-cells, by
 CC combining them with the extracellular portion of p74 and determining the
 CC amount of binding between the candidate compound and p74. Modulation of
 CC CTL activity can be inhibited in a cellular composition containing
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the
 CC extracellular portion of p74, in an amount sufficient to compete with p74
 CC for the binding of the p74 ligand.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25
 QY 1 RIALRY 6
 |||||

RESULT 12
 ID R95422 standard; peptide; 25 AA.
 AC R95422;
 DT 12-NOV-1996 (first entry)
 DE HL38 6084.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytotoxicity; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HL38 6084. These sequences can be used to isolate the protein p74 from
 CC with T-cell activation in mammalian T-cells, and is also immunologically
 CC cross reactive with the heat shock protein Hsc70. p74 is found in a
 CC limited number of cell types, but is particularly expressed on B and T
 CC cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteretic detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25
 QY 1 RIALRY 6
 |||||

RESULT 13
 ID R83090 standard; peptide; 25 AA.
 AC R83090;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.60-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 13; Page 32; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with
 CC a subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25
 QY 1 RIALRY 6
 |||||

RESULT 14
 ID R41205 standard; peptide; 25 AA.
 AC R41205;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN WO9317599-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI: 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 8; Page 53; 61pp; English.
 CC The peptide (or a fragment of at least 10 amino acids, joined at at
 CC least one terminus to a sequence other than that of wild type HLA
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
 CC either by inhibition or stimulation. It can be used for
 CC inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25
|||||
QY 1 RIALRY 6

RESULT 15
ID R83093 standard; peptide; 25 AA.
AC R83093;
DT 16-MAY-1996 (first entry)
DE HLAB38 CTL modulating peptide (B38.6084).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLAB38.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358382/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 13: Page 32: 80pp; English.
CC R83061-R83085, R83090-R83096 and R82907-R82913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLAB38. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.25e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25
|||||
QY 1 RIALRY 6

Search completed: Thu May 22 08:27:40 1997
Job time : 15 secs.

W P E R L H
***** (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Inteligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:28:27 1997; MasPar time 2.70 seconds
Tabular output not generated. 63.421 Million cell updates/sec

Title: >US-08-653-294-5
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 RILLRY 6

Scoring table: PAM 150
Gap 15
Searched: 89912 seqs, 28507787 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 22.859; Variance 32.635; scale 0.700

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description | Pred. No. |
|------------|-------|---------------|--------|----|--------------------------|-----------|
| 1 | 51 | 96.2 | 616 | 10 | prolyl endopeptidase | 6.99e+00 |
| 2 | 48 | 90.6 | 830 | 11 | vacuolar membrane pr | 2.39e+01 |
| 3 | 48 | 90.6 | 832 | 11 | probable membrane pr | 2.39e+01 |
| 4 | 47 | 88.7 | 139 | 13 | VpreB protein - huma | 3.57e+01 |
| 5 | 47 | 88.7 | 142 | 14 | VpreB protein precu | 3.57e+01 |
| 6 | 47 | 88.7 | 142 | 14 | VpreB protein precu | 3.57e+01 |
| 7 | 47 | 88.7 | 145 | 13 | Vpre-B protein - hum | 3.57e+01 |
| 8 | 47 | 88.7 | 437 | 5 | methionine-oxalate-semia | 3.57e+01 |
| 9 | 46 | 86.8 | 137 | 13 | class I histocompati | 5.29e+01 |
| 10 | 46 | 86.8 | 168 | 5 | protein-lysine 6-oxi | 5.29e+01 |
| 11 | 46 | 86.8 | 217 | 9 | neuE protein - Esche | 5.29e+01 |
| 12 | 46 | 86.8 | 218 | 13 | MHC class I HLA-J an | 5.29e+01 |
| 13 | 46 | 86.8 | 274 | 13 | MHC class I HLA-B27 M2+ | 5.29e+01 |
| 14 | 46 | 86.8 | 284 | 6 | MHC class I histocom | 5.29e+01 |
| 15 | 46 | 86.8 | 328 | 14 | MHC H-2K transplanta | 5.29e+01 |
| 16 | 46 | 86.8 | 338 | 13 | MHC HLA-B27-HS - hum | 5.29e+01 |
| 17 | 46 | 86.8 | 345 | 5 | phosphoprotein phosph | 5.29e+01 |
| 18 | 46 | 86.8 | 346 | 5 | phosphoprotein phosph | 5.29e+01 |
| 19 | 46 | 86.8 | 349 | 14 | transcription enhanc | 5.29e+01 |
| 20 | 46 | 86.8 | 362 | 14 | MHC H-2D-K protein - | 5.29e+01 |
| 21 | 46 | 86.8 | 362 | 13 | MHC HLA-Bw47 precurs | 5.29e+01 |

| | | | | | | | |
|----|----|------|------|----|--------|----------------------|----------|
| 22 | 46 | 86.8 | 362 | 6 | C35997 | MHC class I histocom | 5.29e+01 |
| 23 | 46 | 86.8 | 362 | 2 | HLHUB2 | MHC class I histocom | 5.29e+01 |
| 24 | 46 | 86.8 | 362 | 13 | I54289 | MHC HLA-B27d - human | 5.29e+01 |
| 25 | 46 | 86.8 | 362 | 13 | I37485 | human lymphocyte ant | 5.29e+01 |
| 26 | 46 | 86.8 | 365 | 13 | A39481 | serum response facto | 5.29e+01 |
| 27 | 46 | 86.8 | 367 | 6 | S31651 | MHC class I histocom | 5.29e+01 |
| 28 | 46 | 86.8 | 368 | 14 | I68705 | MHC H-2K-w28 protein | 5.29e+01 |
| 29 | 46 | 86.8 | 411 | 1 | OXRTL | protein-lysine 6-oxi | 5.29e+01 |
| 30 | 46 | 86.8 | 411 | 1 | OXMSL | protein-lysine 6-oxi | 5.29e+01 |
| 31 | 46 | 86.8 | 417 | 1 | OXHUL | protein-lysine 6-oxi | 5.29e+01 |
| 32 | 46 | 86.8 | 420 | 13 | A45166 | protein-lysine 6-oxi | 5.29e+01 |
| 33 | 46 | 86.8 | 574 | 5 | A48501 | lysyl oxidase homolo | 5.29e+01 |
| 34 | 46 | 86.8 | 1612 | 16 | S59969 | DNA topoisomerase (A | 5.29e+01 |
| 35 | 46 | 86.8 | 1612 | 6 | S54154 | DNA topoisomerase (A | 5.29e+01 |
| 36 | 46 | 86.8 | 1626 | 6 | A39242 | DNA topoisomerase (A | 5.29e+01 |
| 37 | 46 | 86.8 | 3712 | 16 | S28399 | laminin chain A - fr | 5.29e+01 |
| 38 | 45 | 84.9 | 218 | 8 | S30287 | regulatory protein t | 7.79e+01 |
| 39 | 45 | 84.9 | 218 | 8 | S07359 | regulatory protein t | 7.79e+01 |
| 40 | 45 | 84.9 | 298 | 12 | S53849 | ribosomal protein S3 | 7.79e+01 |
| 41 | 45 | 84.9 | 1203 | 12 | A33165 | finger protein sdc-1 | 7.79e+01 |
| 42 | 44 | 83.0 | 147 | 16 | S60894 | invi protein - Salmo | 1.14e+02 |
| 43 | 44 | 83.0 | 351 | 16 | S62783 | UDPglucose 4-epimera | 1.14e+02 |
| 44 | 44 | 83.0 | 733 | 13 | A57459 | growth factor-stimul | 1.14e+02 |
| 45 | 44 | 83.0 | 735 | 14 | A53300 | S6 protein kinase - | 1.14e+02 |

ALIGNMENTS

RESULT 1
ENTRY JC4084 #type complete
TITLE prolyl endopeptidase (EC 3.4.-.-) - Pyrococcus furiosus
ALTERNATE_NAMES mlr-2 protein
ORGANISM #formal_name Pyrococcus furiosus
DATE 12-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Mar-1996
ACCESSIONS JC4084
REFERENCE JC4084
#authors Robinson, K.A.; Bartley, D.A.; Robb, F.T.; Schreier, H.J.
#journal Gene (1995) 152:103-106
#title A gene from the hyperthermophile Pyrococcus furiosus whose deduced product is homologous to members of the prolyl oligopeptidase family of proteases.

#accession JC4084
#molecule_type DNA
#residues 1-616 #label ROB
#cross-references GB:U08343
KEYWORDS hydrolase; oligopeptidase
FEATURE 477,561,592 #active_site Ser, Asp, His #status predicted
SUMMARY #length 616 #molecular-weight 70867 #checksum 9939

Query Match 96.2%; Score 51; DB 10; Length 616;
Best Local Similarity 83.3%; Pred. No. 6.99e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 334 rvllry 339
|:|:|:|
QY 1 RILLRY 6

RESULT 2
ENTRY S25198 #type complete
TITLE vacuolar membrane protein HMT1 - fission yeast
#(Schizosaccharomyces pombe)
ORGANISM #formal_name Schizosaccharomyces pombe
DATE 28-May-1993 #sequence_revision 28-May-1993 #text_change 20-Jan-1995

ACCESSIONS S25198
REFERENCE S25198
#authors Ortiz, D.F.; Kreppel, L.; Speiser, D.M.; Scheel, G.; McDonald, G.; Ow, D.W.
#journal EMBO J. (1992) 11:3491-3499
#title Heavy metal tolerance in the fission yeast requires an

#accession S25198
 #molecule_type mRNA
 ##residues 1-830 ##label ORT
 ##cross-references EMBL:Z14055

GENETICS

#gene html
 #map_position III
 CLASSIFICATION #superfamily malk protein homology
 KEYWORDS ATP binding; transmembrane protein
 FEATURE

10-31 #domain transmembrane #status predicted #label TM1
 52-71 #domain transmembrane #status predicted #label TM2
 88-108 #domain transmembrane #status predicted #label TM3
 126-146 #domain transmembrane #status predicted #label TM4
 403-423 #domain transmembrane #status predicted #label TM5
 490-511 #domain transmembrane #status predicted #label TM6
 600-794 #domain malk protein homology #label MK1
 SUMMARY #length 830 #molecular-weight 94007 #checksum 7697

Query Match 90.6%; Score 48; DB 11; Length 830;

Best Local Similarity 83.3%; Pred. No. 2.39e+01; Mismatches 0; Indels 0; Gaps 0;

Db 628 rllrf 633

|||||
 QY 1 RILLY 6

RESULT 3

ENTRY S19418 #type complete
 TITLE probable membrane protein YCR106w - yeast (Saccharomyces cerevisiae)
 ORGANISM #formal_name Saccharomyces cerevisiae
 DATE 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-May-1995

ACCESSIONS S19418; S19747

REFERENCE S19415

#authors van der Linden, C.G.; Maurer, C.T.C.; Planta, R.J.; van Vliet-Reedijk, J.C.; Vreken, P.
 #submission submitted to the Protein Sequence Database, March 1992
 #accession S19418

#molecule_type DNA

##residues 1-517 ##label LIN

##cross-references EMBL:X59720

REFERENCE S19376

#authors Grenson, M.; Jauniaux, J.C.; Urrestarazu, L.A.

#submission submitted to the Protein Sequence Database, March 1992

#accession S19747

#molecule_type DNA

##residues 130-832 ##label GRE

##cross-references EMBL:X59720

GENETICS

#map_position 3R
 CLASSIFICATION #superfamily GAL4 zinc binuclear cluster homology
 KEYWORDS transmembrane protein
 FEATURE

10-47

#domain GAL4 zinc binuclear cluster homology #label GAL4
 #domain transmembrane #status predicted #label TM1
 104-121 #domain transmembrane #status predicted #label TM2
 275-292 #domain transmembrane #status predicted #label TM3
 398-414 #domain transmembrane #status predicted #label TM4
 542-558 #domain transmembrane #status predicted #label TM5
 616-632 #domain transmembrane #status predicted #label TM6
 699-715 #domain transmembrane #status predicted #label TM7
 767-783 #domain transmembrane #status predicted #label TM7
 SUMMARY #length 832 #molecular-weight 95689 #checksum 36

Query Match 90.6%; Score 48; DB 11; Length 832;

Best Local Similarity 83.3%; Pred. No. 2.39e+01; Mismatches 0; Indels 0; Gaps 0;

Db 629 rllrf 634

|||||
 QY 1 RILLY 6

RESULT 4

ENTRY S00258 #type complete
 TITLE VpreB protein - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 06-Sep-1996

ACCESSIONS S00258

REFERENCE S00258

#authors Bauer, S.R.; Kudo, A.; Melchers, F.

#journal EMBO J. (1988) 7:111-116

#title Structure and pre-B lymphocyte restricted expression of the VpreB gene in humans and conservation of its structure in other mammalian species.

#cross-references MUID:88196069

#accession S00258

##molecule_type DNA

##residues_type 1-139 ##label BAU

##cross-references EMBL:M34927

GENETICS

#gene GDB:VPREB1

##cross-references GDB:120493

#map_position 22q11.2-22q11.2

#introns 16/1

SUMMARY #length 139 #molecular-weight 15948 #checksum 2257

Query Match

88.7%; Score 47; DB 13; Length 139;

Best Local Similarity 83.3%; Pred. No. 3.57e+01;

Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 66 rllry 71

|||||

QY 1 RILLY 6

RESULT 5

ENTRY A28344 #type complete
 TITLE VpreB protein precursor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 19-May-1989 #sequence_revision 19-May-1989 #text_change 23-Mar-1993

ACCESSIONS A28344

REFERENCE A91077

#authors Kudo, A.; Melchers, F.

#journal EMBO J. (1987) 6:2267-2272

#title A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be selectively expressed in pre-B lymphocytes

#cross-references MUID:88029315

#accession A28344

##molecule_type DNA

##residues 1-142 ##label KUD

##note the authors translated the codon GAG for residue 110 as Gln

FEATURE 20-142

SUMMARY #product VpreB protein #status predicted #label MAT
 #length 142 #molecular-weight 16125 #checksum 8179
 Query Match 88.7%; Score 47; DB 14; Length 142;
 Best Local Similarity 83.3%; Pred. No. 3.57e+01;
 Mismatches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 66 rllry 71

|||||

QY 1 RILLY 6

RESULT 6

ENTRY B28344 #type complete
 TITLE VpreB protein precursor - mouse

```

ORGANISM      #formal_name Mus musculus #common_name house mouse
DATE          19-May-1989 #sequence_revision 19-May-1989 #text_change
ACCESSIONS    B28344
REFERENCE      A91077
#authors      Kudo, A.; Melchers, F.
#journal      EMBO J. (1987) 6:2267-2272
#title        A second gene, VpreB in the lambda-5 locus of the mouse,
              which appears to be selectively expressed in pre-B
              lymphocytes.
#cross-references MIM:88029315
#accession     B28344
#molecule_type DNA
#residues      1-142 #label KUD
#note          the authors translated the codon GAG for residue 110 as
              Gln
FEATURE
20-142        #product VpreB protein #status predicted #label MAT
SUMMARY        #length 142 #molecular-weight 16052 #checksum 7379
Query Match    88.7%; Score 47; DB 14; Length 142;
Best Local Similarity 83.3%; Pred. No. 3.57e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 66 rilly 71
   |::|||
QY 1 RILLY 6

RESULT 7
ENTRY      #type complete
TITLE      Vpre-B protein - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS  I57832
REFERENCE    Foulger, M.; Schiff, C.
#authors     Guelpa-Fonlupt, V.; Bossy, D.; Alzari, P.; Fumoux, F.;
              Foulger, M.; Schiff, C.
#journal     Mol. Immunol. (1994) 31:1099-1108
#title       The human pre-B cell receptor: structural constraints for a
              tentative model of the pseudo-light (psi L) chain.
#cross-references MIM:95021318
#accession   I57832
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues     1-145 #label RES
#cross-references GB:S74019; NID:9693810; CDS_PID:9693811
GENETICS
#introns      16/1
#note         gene name Vpre-B
SUMMARY        #length 145 #molecular-weight 16605 #checksum 5991
Query Match    88.7%; Score 47; DB 13; Length 145;
Best Local Similarity 83.3%; Pred. No. 3.57e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 66 rilly 71
   |::|||
QY 1 RILLY 6

RESULT 8
ENTRY      #type complete
TITLE      methylmalonate-semialdehyde dehydrogenase (acylating) (EC
              1.2.1.27) - Pseudomonas aeruginosa (ATCC 15692)
ORGANISM    #formal_name Pseudomonas aeruginosa
DATE        10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
ACCESSIONS    B42902; S27602
REFERENCE      Steele, M.I.; Lorenz, D.; Hatter, K.; Park, A.; Sokatch, J.R.
#authors      J. Biol. Chem. (1992) 267:13585-13592

```

```

#title        Characterization of the mmsAB operon of pseudomonas
              aeruginosa PAO encoding methylmalonate-semialdehyde
              dehydrogenase and 3-hydroxyisobutyrate dehydrogenase.
#cross-references MIM:92317087
#accession     B42902
#status        preliminary
#molecule_type DNA
#residues      1-497 #label STE
#cross-references EMBL:M84911; NCBI:P107707
GENETICS
#gene          mmsA
#classification #superfamily aldehyde dehydrogenase (NAD+)
              oxidoreductase
KEYWORDS        #length 497 #molecular-weight 53663 #checksum 4590
SUMMARY
Query Match    88.7%; Score 47; DB 5; Length 497;
Best Local Similarity 66.7%; Pred. No. 3.57e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 68 rilly 73
   |::|||
QY 1 RILLY 6

RESULT 9
ENTRY      #type fragment
TITLE      class I histocompatibility antigen - chimpanzee (fragment)
ORGANISM    #formal_name Pan troglodytes #common_name chimpanzee
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS  I80174
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
              A.L.; Bontrup, R.E.; Watkins, D.I.
#authors     Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#journal     A uniquely high level of recombination at the HLA-B locus.
#title
#cross-references MIM:94286544
#accession   I80174
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues     1-137 #label RES
#cross-references EMBL:005585; NID:g454787; CDS_PID:g454788
SUMMARY        #length 137 #checksum 5064
Query Match    86.8%; Score 46; DB 13; Length 137;
Best Local Similarity 83.3%; Pred. No. 5.29e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 44 rilly 49
   |::|||
QY 1 RILLY 6

RESULT 10
ENTRY      #type fragments
TITLE      protein-lysine 6-oxidase (EC 1.4.3.13) - pig (fragments)
ALTERNATE_NAMES lysyl oxidase
ORGANISM    #formal_name Sus scrofa domestica #common_name domestic pig
DATE        27-Oct-1995 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS    S54337
REFERENCE      S54337
#authors      Crouchaw, A.D.; Fothergill-Gilmore, L.A.; Hulmes, D.J.S.
#journal      Biochem. J. (1995) 306:279-284
#title        The proteolytic processing site of the precursor of lysyl
              oxidase.
#accession     S54337
#molecule_type protein
#residues      1-168 #label CRO
#note          the amino end of the mature protein was determined after
              unblocking; the nature of the blocking group was not
              determined
FUNCTION

```

#description using molecular oxygen catalyzes the oxidative deamination of peptidyl-lysine to peptidyl-allysine, ammonium and hydrogen peroxide

#pathway collagen biosynthesis; elastin biosynthesis
CLASSIFICATION superfamily protein-lysine 6-oxidase
KEYWORDS blocked amino end; copper; extracellular protein; glycoprotein; oxidoreductase; quinoprotein

FEATURE
1 #modified_site blocked amino end (Asp) #status experimental

SUMMARY #length 188 #checksum 7344

Query Match 86.8%; Score 46; DB 5; Length 168;

Best Local Similarity 66.7%; Pred. No. 5.29e+01;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 85 rvllrf 90

|||||

QY 1 RILLY 6

RESULT 11

ENTRY A42644 #type fragment

TITLE neuE protein - Escherichia coli (fragment)

ORGANISM #formal_name Escherichia coli

DATE 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change

ACCESSIONS A42644; S21890

REFERENCE A42644

#authors Steenbergen, S.M.; Wrona, T.J.; Vimr, E.R.

#journal J. Bacteriol. (1992) 174:1099-1108

#title Functional analysis of the sialyltransferase complexes in

Escherichia coli K1 and K92.

#cross-references MUID:92138601

#accession A42644

##status preliminary

##molecule_type DNA

##residues 1-217 #label STE

##cross-references NCBI:79370; NCBI:79375

##experimental_source K1, strain EV1

##note sequence inconsistent with the nucleotide translation

##note sequence extracted from NCBI backbone

REFERENCE S21890

#authors Weisgerber, C.

#submission submitted to the EMBL Data Library, July 1991

#accession S21890

##status preliminary

##molecule_type DNA

##residues 35-217 #label WEI

##cross-references EMBL:X60598

GENETICS

#gene neuE

SUMMARY #length 217 #checksum 1066

Query Match 86.8%; Score 46; DB 9; Length 217;

Best Local Similarity 66.7%; Pred. No. 5.29e+01;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 207 kvllry 212

|||||

QY 1 RILLY 6

RESULT 12

ENTRY I72808 #type complete

TITLE MHC class I HLA-J antigen - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change

ACCESSIONS I72808

REFERENCE I56139

#authors

Messer, G.; Zemmour, J.; Orr, H.T.; Parham, P.; Weiss, E.H.;

Girdlestone, J.

#journal J. Immunol. (1992) 148:4043-4053

#title HLA-J, a second inactivated class I HLA gene related to HLA-G and HLA-A. Implications for the evolution of the HLA-A-related genes.

#cross-references MUID:92291530

#accession I72808

##status preliminary; translated from GB/EMBL/DBJ

##molecule_type DNA

##residues 1-218 #label RES

##cross-references GB:M80470; NID:9808907; CDS_PID:g553586

SUMMARY #length 218 #molecular_weight 24840 #checksum 7887

Query Match 86.8%; Score 46; DB 13; Length 218;

Best Local Similarity 83.3%; Pred. No. 5.29e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 102 rllly 107

|||||

QY 1 RILLY 6

RESULT 13

ENTRY I55965 #type fragment

TITLE HLA-B*27 M2+ - human (fragment)

ORGANISM #formal_name Homo sapiens #common_name man

DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change

ACCESSIONS I55965

REFERENCE I55965

#authors Coppin, H.L.; McDevitt, H.O.

#journal J. Immunol. (1986) 137:2168-2172

#title Absence of polymorphism between HLA-B*27 genomic exon

sequences isolated from normal donors and ankylosing

spondylitis patients.

#cross-references MUID:87009855

#accession I55965

##status preliminary; translated from GB/EMBL/DBJ

##molecule_type DNA

##residues 1-274 #label RES

##cross-references GB:M14013; NID:9187743; CDS_PID:g187744

SUMMARY #length 274 #checksum 8911

Query Match 86.8%; Score 46; DB 13; Length 274;

Best Local Similarity 83.3%; Pred. No. 5.29e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 rllly 84

|||||

QY 1 RILLY 6

RESULT 14

ENTRY A45840 #type fragment

TITLE MHC class I histocompatibility antigen RT-BM1 alpha chain -

rat (fragment)

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change

ACCESSIONS A45840

REFERENCE A45840

#authors Parker, K.E.; Carter, C.A.; Fabre, J.W.

#journal Immunogenetics (1990) 31:211-214

#title A rat class I cDNA clone with an Alu-like sequence and

mapping to two genes in RT1.C/E.

#accession A45840

##status preliminary

##molecule_type mRNA

##residues 1-284 #label PAR

##cross-references GB:X16979

CLASSIFICATION #superfamily class I histocompatibility antigen;

immunoglobulin homology

FEATURE

137-202

#domain immunoglobulin homology #label IMM

```

SUMMARY      #length 284  #checksum 7381
Query Match   86.8%; Score 46; DB 6; Length 284;
Best Local Similarity 83.3%; Pred.No. 5.29e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 20 rllry 25
   | | | | |
QY 1 RLLRY 6

RESULT 15
ENTRY
TITLE      #type fragment
ORGANISM   MHC H-2K transplantation antigen - mouse (fragment)
DATE       #formal_name Mus musculus #common_name house mouse
           02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
           02-Aug-1996
ACCESSIONS I54414
REFERENCE  I54414
#authors   Morita, T.; Delarbre, C.; Kress, M.; Kourilsky, P.; Gachelin,
           G.
#journal   Immunogenetics (1985) 21:367-383
#title     An H-2K gene of the t-w32 mutant at the T/t complex is a
           close parent of an H-2K-q gene.
#cross-references MUID:85206119
#accession  I54414
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-328 #label RES
#cross-references GB:M14827; NID:g199550; CDS_PID:g387471
#length 328 #checksum 6118
SUMMARY

Query Match   86.8%; Score 46; DB 14; Length 328;
Best Local Similarity 83.3%; Pred.No. 5.29e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 60 rllry 65
   | | | | |
QY 1 RLLRY 6

```

Search completed: Thu May 22 08:28:46 1997
Job time : 19 secs.

THIS PAGE BLANK (USPTO)

MPERCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:29:04 1997; MasPar time 1.90 Seconds
Tabular output not generated. 34.326 Million cell updates/sec

Title: >US-08-653-294-5
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 RILLRY 6

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 16.452; Variance 46.284; scale 0.355

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------|--------|--------|-----------------------|-----------|
| 1 | 53 | 100.0 | 10 16 | R83096 | HLA-B2702 CTL modul | 1.30e+01 |
| 2 | 47 | 88.7 | 125 1 | P80289 | Human Vpre-B protein. | 6.38e+01 |
| 3 | 47 | 88.7 | 142 1 | P83001 | V preB-2 protein. | 6.38e+01 |
| 4 | 47 | 88.7 | 142 1 | P80288 | V preB-1 protein. | 6.38e+01 |
| 5 | 46 | 86.8 | 10 18 | R95423 | HLA-B2705.75-84. | 8.26e+01 |
| 6 | 46 | 86.8 | 10 8 | R41212 | Peptide fragment of C | 8.26e+01 |
| 7 | 46 | 86.8 | 10 16 | R83075 | HLA-B2702 CTL modul | 8.26e+01 |
| 8 | 46 | 86.8 | 17 13 | R71425 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 9 | 46 | 86.8 | 17 13 | R71425 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 10 | 46 | 86.8 | 17 13 | R71443 | Human (Phe74)-HLA-B27 | 8.26e+01 |
| 11 | 46 | 86.8 | 17 13 | R71440 | Human MHC 1 and HLA f | 8.26e+01 |
| 12 | 46 | 86.8 | 17 13 | R71433 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 13 | 46 | 86.8 | 17 13 | R71426 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 14 | 46 | 86.8 | 17 13 | R71428 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 15 | 46 | 86.8 | 24 13 | R71424 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 16 | 46 | 86.8 | 24 13 | R71434 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 17 | 46 | 86.8 | 24 13 | R71436 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 18 | 46 | 86.8 | 24 13 | R71427 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 19 | 46 | 86.8 | 24 13 | R71435 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 20 | 46 | 86.8 | 25 18 | R95417 | HLA-B2705.60-84. | 8.26e+01 |

| | | | | | | |
|----|----|------|--------|--------|-----------------------|----------|
| 21 | 46 | 86.8 | 25 13 | R71420 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 22 | 46 | 86.8 | 25 3 | R20116 | MHC Class I-derived p | 8.26e+01 |
| 23 | 46 | 86.8 | 25 8 | R41221 | Peptide fragment of H | 8.26e+01 |
| 24 | 46 | 86.8 | 25 13 | R69619 | MHC-1 peptide DK-(61- | 8.26e+01 |
| 25 | 46 | 86.8 | 25 16 | R83091 | HLA-B2702 CTL modul | 8.26e+01 |
| 26 | 46 | 86.8 | 337 2 | P70590 | Sequence of the human | 8.26e+01 |
| 27 | 46 | 86.8 | 362 2 | P70155 | Sequence encoded by g | 8.26e+01 |
| 28 | 46 | 86.8 | 365 9 | R50040 | xMEF2. | 8.26e+01 |
| 29 | 45 | 84.9 | 24 13 | R71438 | Human MHC 1 alpha 1 d | 1.07e+02 |
| 30 | 44 | 83.0 | 306 12 | R63791 | Aspergillus aculeatus | 1.38e+02 |
| 31 | 44 | 83.0 | 740 18 | R95912 | Mutant insulin-stimul | 1.38e+02 |
| 32 | 44 | 83.0 | 740 18 | R95911 | Insulin-stimulated pr | 1.38e+02 |
| 33 | 43 | 81.1 | 415 3 | R20104 | ERK2. | 1.77e+02 |
| 34 | 43 | 81.1 | 534 13 | R69720 | Cyclic-GMP stimulated | 1.77e+02 |
| 35 | 43 | 81.1 | 534 5 | R28404 | 63 kD Cam PDE from cl | 1.77e+02 |
| 36 | 42 | 79.2 | 10 18 | R95425 | HLA-B2702.75-84(D). | 2.28e+02 |
| 37 | 42 | 79.2 | 10 16 | R95413 | Alphal-helix of HLA-B | 2.28e+02 |
| 38 | 42 | 79.2 | 10 16 | R83062 | HLA-B2702 CTL modul | 2.28e+02 |
| 39 | 42 | 79.2 | 12 18 | R95429 | HLA-B2702 84-79-84 pa | 2.28e+02 |
| 40 | 42 | 79.2 | 20 18 | R95428 | HLA-B2702 84-75-84 pa | 2.28e+02 |
| 41 | 42 | 79.2 | 20 16 | R92908 | HLA-B2702 CTL modul | 2.28e+02 |
| 42 | 42 | 79.2 | 25 18 | R95416 | HLA-B2702.60-84. | 2.28e+02 |
| 43 | 42 | 79.2 | 25 18 | R95422 | HLAB38.6084. | 2.28e+02 |
| 44 | 42 | 79.2 | 108 18 | R93159 | Murine monoclonal ant | 2.28e+02 |
| 45 | 42 | 79.2 | 595 8 | R41359 | Tumour associated 90K | 2.28e+02 |

ALIGNMENTS

RESULT 1
ID R83096 standard; peptide; 10 AA.
AC R83096:
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84(L)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STED) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-359582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 14; Page 34; 80pp; English.
CC R83061-R83085; R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with
CC a subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.30e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 5 rillyr 10
QY 1 RILLRY 6
RESULT 2
ID P80289 standard; protein; 125 AA.

AC P80289;
 DT 07-DEC-1990 (first entry)
 DE Human Vpre-B protein.
 KW Pre-B cells; non-T acute lymphoblast leukaemia.
 PN EP-269127-A.
 PD 01-JUN-1988.
 PF 27-NOV-1987; 117619.
 PR 27-NOV-1986; GB-028433.
 PR 14-JUL-1987; GB-016497.
 PR 14-OCT-1987; GB-024100.
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 PI Bauer SR, Kudo A, Melchers GF, Sakaguchi N;
 DR WPI; 88-148947/22.
 DR N-PSDB; N80476.
 PT Nucleotide sequence selectively expressed in pre-B cells - used
 PT in probes for determining non-T acute lymphoblast leukaemia and
 PT for prepn. of polypeptide(s)
 PS Disclosure; pp; English.
 CC This is encoded by the human pre-B gene which differs from the
 CC mouse pre-B-2 gene (of N82441) at several posns. The gene is also
 CC selectively expressed in pre-B cell lines. Its pattern of express-
 CC ion follows that of Vpre-B1 and lambda-5 in the mouse.
 CC See also N80470-75, N80475 and N82441-42.
 SQ Sequence 125 AA;
 Query Match 88.7%; Score 47; DB 1; Length 125;
 Best Local Similarity 83.3%; Pred. No. 6.38e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 52 rllly 57
 I:||||
 QY 1 RILLY 6
 RESULT 3
 ID P83001 standard; protein; 142 AA.
 AC P83001;
 DT 07-DEC-1990 (first entry)
 DE V pre-B-2 protein.
 KW Pre-B cells; non-T acute lymphoblast leukaemia.
 PN EP-269127-A.
 PD 01-JUN-1988.
 PF 27-NOV-1987; 117619.
 PR 27-NOV-1986; GB-028433.
 PR 14-JUL-1987; GB-016497.
 PR 14-OCT-1987; GB-024100.
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 PI Bauer SR, Kudo A, Melchers GF, Sakaguchi N;
 DR WPI; 88-148947/22.
 DR N-PSDB; N82441.
 PT Nucleotide sequence selectively expressed in pre-B cells - used
 PT in probes for determining non-T acute lymphoblast leukaemia and
 PT for prepn. of polypeptide(s)
 PS Disclosure; pp; English.
 CC This is encoded by the genomic form of the variable region pre-B-2
 CC sequence. The gene is not rearranged during pre-B cell development.
 CC This protein may associate with itself or with heavy chain V domains
 CC expressed in pre-B cells. The gene is expressed only in pre-B cell lines.
 CC See also N80470-75, N80476-77 and N82442.
 SQ Sequence 142 AA;
 Query Match 88.7%; Score 47; DB 1; Length 142;
 Best Local Similarity 83.3%; Pred. No. 6.38e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 66 rllly 71
 I:||||
 QY 1 RILLY 6
 RESULT 4
 ID P80288 standard; protein; 142 AA.
 AC P80288;

DT 07-DEC-1990 (first entry)
 DE V pre-B-1 protein.
 KW Pre-B cells; non-T acute lymphoblast leukaemia; ss;
 PN EP-269127-A.
 PD 01-JUN-1988.
 PF 27-NOV-1987; 117619.
 PR 27-NOV-1986; GB-028433.
 PR 14-JUL-1987; GB-016497.
 PR 14-OCT-1987; GB-024100.
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 PI Bauer SR, Kudo A, Melchers GF, Sakaguchi N;
 DR WPI; 88-148947/22.
 DR N-PSDB; N80475.
 PT Nucleotide sequence selectively expressed in pre-B cells - used
 PT in probes for determining non-T acute lymphoblast leukaemia and
 PT for prepn. of polypeptide(s)
 PS Disclosure; pp; English.
 CC This is encoded by the genomic form of the variable region pre-B-1
 CC sequence. The gene is not rearranged during pre-B cell development
 CC and is 4.6 kb upstream of the lambda-5 gene. This protein can
 CC associate with itself or with heavy chain V domains expressed in
 CC pre-B cells. Vpre-B-1 and lambda-5 form a complete V domain via
 CC non-covalent bonds. The gene is expressed only in pre-B cell lines.
 CC See also N80470-74, N80476-77 and N82441-42.
 SQ Sequence 142 AA;
 Query Match 88.7%; Score 47; DB 1; Length 142;
 Best Local Similarity 83.3%; Pred. No. 6.38e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 66 rllly 71
 I:||||
 QY 1 RILLY 6
 RESULT 5
 ID R95423 standard; peptide; 10 AA.
 AC R95423;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2705.75-84.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-41.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2705.75-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the

CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.

SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 18; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10

1 |||||

QY 1 RILLY 6

RESULT 6

ID R41212 standard; peptide; 10 AA.

AC R41212;

DT 15-MAR-1994 (first entry)

DE Peptide fragment of Class I HLA peptide.

KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;

OS Synthetic.

PN W09317699-A.

PD 16-SEP-1993.

PF 25-FEB-1993; U01758.

PR 02-MAR-1992; US-844716.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger CA, Krensky AM;

DR WPI: 93-303134/38.

PT New peptide(s) based on Class I HLA antigen domains - used for

PT modulating cytotoxic T-lymphocyte activity towards targets

PS Claim 11; Page 54; 61pp; English.

CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)

CC activity, either by inhibition or stimulation. It can be used

CC for inhibiting CTL toxicity in transplantations, for inducing CTL

CC activity in parasitic diseases and neoplasia and in studies on viral

CC infection. The peptide can also be used for identifying CTLs which

CC bind to it and removing subsets of CTLs from a T-cell composition.

CC This peptide sequence is more commonly found within larger peptide

CC compounds of not more than 30 amino acids in length.

SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 8; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10

1 |||||

QY 1 RILLY 6

RESULT 7

ID R83075 standard; peptide; 10 AA.

AC R83075;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI: 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 14; Page 34; 80pp; English.

CC R83061-R83085, R83090-R83096 and R82907-R82913 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC corresponds to residues 75-84 of the alpha-1 domain of the class

CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.

SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 16; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10

1 |||||

QY 1 RILLY 6

RESULT 8

ID R71425 standard; peptide; 17 AA.

AC R71425;

DT 12-OCT-1995 (first entry)

DE Human MHC 1 alpha 1 domain peptide Dk-(69-85).

KW Major histocompatibility complex class 1; MHC 1; cell receptor;

KW alpha 1 domain; peptide Dk-(62-85); interaction modulation;

OS Homo sapiens.

PN W09505189-A.

PD 23-FEB-1995.

PF 12-AUG-1994; U09189.

PR 12-AUG-1993; US-105416.

PA (REGC) UNIV CALIFORNIA.

PI Goldstein A, Goodenow RS, Olsson L;

DR WPI: 95-098577/13.

PT Regulating cell surface receptor response - by modulating

PT interaction between MHC class I antigen and the cell surface

PT receptor

PS Example 4; Page 45; 103pp; English.

CC R71424-R71438 are human major histocompatibility complex class 1

CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they

CC were used to modulate interactions between MHC 1 and cell surface

CC receptors. Via competitive inhibition the peptides diminish the

CC receptors response, this feature may be useful for the treatment

CC of neoplasias, lupus erythematosus and arthritis.

SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16

1 |||||

QY 1 RILLY 6

RESULT 9

ID R71442 standard; peptide; 17 AA.

AC R71442;

DT 12-OCT-1995 (first entry)

DE Human HLA-B27-(62-85) antigen derived peptide.

KW Human HLA-B27-(62-85) antigen derived peptide; cell receptor;

KW interaction modulation; arthritis; neoplasias; lupus erythematosus.

OS Homo sapiens.

PN W09505189-A.

PD 23-FEB-1995.

PF 12-AUG-1994; U09189.

PR 12-AUG-1993; US-105416.

PA (REGC) UNIV CALIFORNIA.

PI Goldstein A, Goodenow RS, Olsson L;

DR WPI: 95-098577/13.

PT Regulating cell surface receptor response - by modulating

PT interaction between MHC class I antigen and the cell surface

PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71439-R71443 are human major histocompatibility complex class 1
 CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
 CC They were used to modulate interactions between MHC 1/HLA and cell
 CC surface receptors. Via competitive inhibition the peptides diminish
 CC the receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16
 | | | | |
 QY 1 RILLY 6

RESULT 10
 ID R71443 standard; peptide; 17 AA.
 AC R71443;
 DT 12-OCT-1995 (first entry)
 DE Human [Phe74]-HLA-B27-(62-85) antigen derived peptide.
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;
 KW interaction modulation; arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN WO9505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI; 95-098577/13.
 DT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71439-R71443 are human major histocompatibility complex class 1
 CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
 CC They were used to modulate interactions between MHC 1/HLA and cell
 CC surface receptors. Via competitive inhibition the peptides diminish
 CC the receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16
 | | | | |
 QY 1 RILLY 6

RESULT 11
 ID R71440 standard; peptide; 17 AA.
 AC R71440;
 DT 12-OCT-1995 (first entry)
 DE Human MHC 1 and HLA fusion peptide HLA-A2-(69-76)Dk-(77-85).
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;
 KW alpha 1 domain; fusion peptide HLA-A2-(69-76)Dk-(77-85);
 KW interaction modulation; arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN WO9505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI; 95-098577/13.
 DT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface

PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71439-R71443 are human major histocompatibility complex class 1
 CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
 CC They were used to modulate interactions between MHC 1/HLA and cell
 CC surface receptors. Via competitive inhibition the peptides diminish
 CC the receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16
 | | | | |
 QY 1 RILLY 6

RESULT 12
 ID R71433 standard; peptide; 17 AA.
 AC R71433;
 DT 12-OCT-1995 (first entry)
 DE Human MHC 1 alpha 1 domain peptide [Ala85]-Dk-(69-85).
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;
 KW alpha 1 domain; peptide [Ala85]-Dk-(69-85); interaction modulation;
 KW arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN WO9505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI; 95-098577/13.
 DT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71439-R71443 are human major histocompatibility complex class 1
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
 CC were used to modulate interactions between MHC 1 and cell surface
 CC receptors. Via competitive inhibition the peptides diminish the
 CC receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16
 | | | | |
 QY 1 RILLY 6

RESULT 13
 ID R71426 standard; peptide; 17 AA.
 AC R71426;
 DT 12-OCT-1995 (first entry)
 DE Human MHC 1 alpha 1 domain peptide [Ala71]-Dk-(69-85).
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;
 KW alpha 1 domain; peptide [Ala71]-Dk-(69-85); interaction modulation;
 KW arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN WO9505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI; 95-098577/13.
 DT Regulating cell surface receptor response - by modulating

PT interaction between MHC class I antigen and the cell surface
 PS receptor
 CC Example 4; Page 45; 103pp; English.
 CC R71424-R71438 are human major histocompatibility complex class I
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
 CC were used to modulate interactions between MHC 1 and cell surface
 CC receptors. Via competitive inhibition the peptides diminish the
 CC receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
 Best Local Similarity 83.3%; Pred. NO. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16
 | | | | |
 QY 1 RILLY 6

RESULT 14
 ID R71428 standard; peptide; 17 AA.
 AC R71428;
 DT 12-OCT-1995 (first entry)
 DE Human MHC 1 alpha 1 domain peptide [Ala78]-Dk-(69-85).
 KW Major histocompatibility complex class I; MHC 1; cell receptor;
 KW alpha 1 domain; peptide [Ala78]-Dk-(69-85); interaction modulation;
 KW arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN WO9505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI; 95-098577/13.
 PT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71424-R71438 are human major histocompatibility complex class I
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
 CC were used to modulate interactions between MHC 1 and cell surface
 CC receptors. Via competitive inhibition the peptides diminish the
 CC receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
 Best Local Similarity 83.3%; Pred. NO. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16
 | | | | |
 QY 1 RILLY 6

RESULT 15
 ID R71424 standard; peptide; 24 AA.
 AC R71424;
 DT 12-OCT-1995 (first entry)
 DE Human MHC 1 alpha 1 domain peptide Dk-(62-85).
 KW Major histocompatibility complex class I; MHC 1; cell receptor;
 KW alpha 1 domain; peptide Dk-(62-85); interaction modulation;
 KW arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN WO9505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI; 95-098577/13.

PT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71424-R71438 are human major histocompatibility complex class I
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
 CC were used to modulate interactions between MHC 1 and cell surface
 CC receptors. Via competitive inhibition the peptides diminish the
 CC receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 24 AA;

Query Match 86.8%; Score 46; DB 13; Length 24;
 Best Local Similarity 83.3%; Pred. NO. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rtllry 23
 | | | | |
 QY 1 RILLY 6

Search completed: Thu May 22 08:29:12 1997
 Job time : 8 secs.

THIS PAGE BLANK (USPTO)

M A I N

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:43:51 1997; MasPar time 1.74 Seconds
37.653 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-5
Description: (1-6) from US08653294.pep
Perfect score: 53

Sequence: 1 RILLRY 6

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 16.452; Variance 46.284; scale 0.355

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|-----------------------|-----------|
| 1 | 53 | 100.0 | 10 16 | R83096 | HLA-B2702 CTL modul | 1.30e+01 |
| 2 | 46 | 86.8 | 10 18 | R95423 | HLA-B2705.75-84. | 8.26e+01 |
| 3 | 46 | 86.8 | 10 16 | R41212 | Peptide fragment of C | 8.26e+01 |
| 4 | 46 | 86.8 | 10 16 | R83075 | HLA-B2702 CTL modul | 8.26e+01 |
| 5 | 46 | 86.8 | 17 13 | R71425 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 6 | 46 | 86.8 | 17 13 | R71442 | Human HLA-B27-(62-85) | 8.26e+01 |
| 7 | 46 | 86.8 | 17 13 | R71443 | Human (Phe74)-HLA-B27 | 8.26e+01 |
| 8 | 46 | 86.8 | 17 13 | R71440 | Human MHC 1 and HLA f | 8.26e+01 |
| 9 | 46 | 86.8 | 17 13 | R71433 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 10 | 46 | 86.8 | 17 13 | R71426 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 11 | 46 | 86.8 | 17 13 | R71428 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 12 | 46 | 86.8 | 24 13 | R71424 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 13 | 46 | 86.8 | 24 13 | R71434 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 14 | 46 | 86.8 | 24 13 | R71436 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 15 | 46 | 86.8 | 24 13 | R71427 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 16 | 46 | 86.8 | 24 13 | R71435 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 17 | 46 | 86.8 | 25 18 | R95417 | HLA-B2705.60-84. | 8.26e+01 |
| 18 | 46 | 86.8 | 25 13 | R71420 | Human MHC 1 alpha 1 d | 8.26e+01 |
| 19 | 46 | 86.8 | 25 3 | R20116 | MHC Class I-derived p | 8.26e+01 |

| | | | | | | |
|----|----|------|-------|--------|-----------------------|----------|
| 20 | 46 | 86.8 | 25 8 | R41221 | Peptide fragment of H | 8.26e+01 |
| 21 | 46 | 86.8 | 25 13 | R69619 | MHC-I peptide Dk-(61- | 8.26e+01 |
| 22 | 46 | 86.8 | 25 16 | R83091 | HLA-B2702 CTL modul | 8.26e+01 |
| 23 | 45 | 84.9 | 24 13 | R71438 | Human MHC 1 alpha 1 d | 1.07e+02 |
| 24 | 42 | 79.2 | 10 18 | R95425 | HLA-B2702.75-84(D). | 2.28e+02 |
| 25 | 42 | 79.2 | 10 18 | R95413 | Alphal-helix of HLA-B | 2.28e+02 |
| 26 | 42 | 79.2 | 10 16 | R83062 | HLA-B2702 CTL modul | 2.28e+02 |
| 27 | 42 | 79.2 | 12 18 | R95429 | HLA-B2702 84-79-84 pa | 2.28e+02 |
| 28 | 42 | 79.2 | 20 18 | R95428 | HLA-B2702 84-75-84 pa | 2.28e+02 |
| 29 | 42 | 79.2 | 20 16 | R92908 | HLA-B2702 CTL modul | 2.28e+02 |
| 30 | 42 | 79.2 | 25 18 | R95416 | HLA-B2702.60-84. | 2.28e+02 |
| 31 | 42 | 79.2 | 25 18 | R95422 | HLA-B2702.60-84. | 2.28e+02 |

Note: Post-processor removed 14 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID R83096 standard; peptide; 10 AA.
AC R83096:
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84(L)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 14; Page 34; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with
CC a subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA;

RESULT 2
ID R95423 standard; peptide; 10 AA.
AC R95423:
DT 12-NOV-1996 (first entry)
DE HLA-B2705.75-84.
KW HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.

PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC R5413, and R5415-R5431 represent palindromes and fragments of
 CC human-leukocyte-associated antigens. This sequence represents the
 CC HLA-B2705.75-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R5416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 18; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rllly 10
 | | | |
 QY 1 RILLY 6

RESULT 3

ID R41212 standard; peptide; 10 AA.

AC R41212;

DT 15-MAR-1994 (first entry)

DE Peptide fragment of Class I HLA peptide.

KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;

KW parasitic disease; cytotoxic T lymphocyte; modulation.

OS Synthetic.

PN W09317699-A.

PD 16-SEP-1993.

PF 25-FEB-1993; U01758.

PR 02-MAR-1992; US-844716.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger CA, Krensky AM;

DR WPI; 93-303134/38.

DT New peptide(s) based on Class I HLA antigen domains - used for

PT modulating cytotoxic T-lymphocyte activity towards targets

PS Claim 11; Page 54; 61pp; English.

CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)

CC activity, either by inhibition or stimulation. It can be used

CC for inhibiting CTL toxicity in transplantations, for inducing CTL

CC activity in parasitic diseases and neoplasia and in studies on viral

CC infection. The peptide can also be used for identifying CTLs which

CC bind to it and removing subsets of CTLs from a T-cell composition.

CC This peptide sequence is more commonly found within larger peptide

CC compounds of not more than 30 amino acids in length.

SQ Sequence 10 AA;

Db 5 rllly 10

| | | |

QY 1 RILLY 6

Query Match 86.8%; Score 46; DB 8; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4

ID R83075 standard; peptide; 10 AA.

AC R83075;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 14; Page 34; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC corresponds to residues 75-84 of the alpha-1 domain of the class

CC I MHC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 16; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rllly 10
 | | | |
 QY 1 RILLY 6

RESULT 5

ID R71425 standard; peptide; 17 AA.

AC R71425;

DT 12-OCT-1995 (first entry)

DE Human MHC 1 alpha 1 domain peptide Dk-(69-85).

KW Major histocompatibility complex class I; MHC 1; cell receptor;

KW alpha 1 domain; peptide Dk-(62-85); interaction modulation;

KW arthritis; neoplasias; lupus erythematosus.

OS Homo sapiens.

PN W09505189-A.

PD 23-FEB-1995.

PF 12-AUG-1994; U09189.

PR 12-AUG-1993; US-105416.

PA (REGC) UNIV CALIFORNIA.

PI Goldstein A, Goodenow RS, Olsson L;

DR WPI; 95-098577/13.

PT Regulating cell surface receptor response - by modulating

PT interaction between MHC class I antigen and the cell surface

PT receptor

PS Example 4; Page 45; 103pp; English.

CC R71424-R71438 are human major histocompatibility complex class 1

CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they

CC were used to modulate interactions between MHC 1 and cell surface

CC receptors. Via competitive inhibition the peptides diminish the

CC receptors response, this feature may be useful for the treatment

CC of neoplasias, lupus erythematosus and arthritis.

SQ Sequence 17 AA;

Db 5 rllly 10

| | | |

QY 1 RILLY 6

Query Match 86.8%; Score 46; DB 13; Length 17;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16
1 |||||
Qy 1 RILLRY 6

RESULT 6
ID R71442 standard; peptide; 17 AA.
AC R71442;
DT 12-OCT-1995 (first entry)
DE Human HLA-B27-(62-85) antigen derived peptide.
KW Human HLA-B27-(62-85) antigen derived peptide; cell receptor;
KW interaction modulation; arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PF 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71439-R71443 are human major histocompatibility complex class 1
CC (MHC I) alpha 1 domain and HLA derived peptides and fusion peptides.
CC They were used to modulate interactions between MHC I/HLA and cell
CC surface receptors. Via competitive inhibition the peptides diminish
CC the receptors response. This feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16
1 |||||
Qy 1 RILLRY 6

RESULT 7
ID R71443 standard; peptide; 17 AA.
AC R71443;
DT 12-OCT-1995 (first entry)
DE Human [Phe74]-HLA-B27-(62-85) antigen derived peptide.
KW Human [Phe74]-HLA-B27-(62-85) antigen derived peptide; cell receptor;
KW interaction modulation; arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PF 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71439-R71443 are human major histocompatibility complex class 1
CC (MHC I) alpha 1 domain and HLA derived peptides and fusion peptides.
CC They were used to modulate interactions between MHC I/HLA and cell
CC surface receptors. Via competitive inhibition the peptides diminish
CC the receptors response. This feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16
1 |||||
Qy 1 RILLRY 6

RESULT 8
ID R71440 standard; peptide; 17 AA.
AC R71440;
DT 12-OCT-1995 (first entry)
DE Human MHC I and HLA fusion peptide HLA-A2-(69-76)Dk-(77-85).
KW Major histocompatibility complex class 1; MHC I; cell receptor;
KW alpha 1 domain; fusion peptide HLA-A2-(69-76)Dk-(77-85);
KW interaction modulation; arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PF 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71439-R71443 are human major histocompatibility complex class 1
CC (MHC I) alpha 1 domain and HLA derived peptides and fusion peptides.
CC They were used to modulate interactions between MHC I/HLA and cell
CC surface receptors. Via competitive inhibition the peptides diminish
CC the receptors response. This feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16
1 |||||
Qy 1 RILLRY 6

RESULT 9
ID R71433 standard; peptide; 17 AA.
AC R71433;
DT 12-OCT-1995 (first entry)
DE Human MHC I alpha 1 domain peptide [Ala85]-Dk-(69-85).
KW Major histocompatibility complex class 1; MHC I; cell receptor;
KW alpha 1 domain; peptide [Ala85]-Dk-(69-85); interaction modulation;
KW arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PF 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC I) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC I and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllry 16
| | | |
QY 1 RILLY 6

RESULT 10

ID R71426 standard; peptide; 17 AA.
AC R71426;
DT 12-OCT-1995 (first entry)
DE Human MHC 1 alpha 1 domain peptide [Ala71]-Dk-(69-85).
KW Major histocompatibility complex class 1; MHC 1; cell receptor;
KW alpha 1 domain; peptide [Ala71]-Dk-(69-85); interaction modulation;
KW arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PF 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllry 16
| | | |
QY 1 RILLY 6

RESULT 11

ID R71428 standard; peptide; 17 AA.
AC R71428;
DT 12-OCT-1995 (first entry)
DE Human MHC 1 alpha 1 domain peptide [Ala78]-Dk-(69-85).
KW Major histocompatibility complex class 1; MHC 1; cell receptor;
KW alpha 1 domain; peptide [Ala78]-Dk-(69-85); interaction modulation;
KW arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PF 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllry 16
| | | |
QY 1 RILLY 6

RESULT 12

ID R71424 standard; peptide; 24 AA.
AC R71424;
DT 12-OCT-1995 (first entry)
DE Human MHC 1 alpha 1 domain peptide Dk-(62-85).
KW Major histocompatibility complex class 1; MHC 1; cell receptor;
KW alpha 1 domain; peptide Dk-(62-85); interaction modulation;
KW arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PF 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 24 AA;

Query Match 86.8%; Score 46; DB 13; Length 24;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rllry 23
| | | |
QY 1 RILLY 6

RESULT 13

ID R71434 standard; peptide; 24 AA.
AC R71434;
DT 12-OCT-1995 (first entry)
DE Human MHC 1 alpha 1 domain peptide [Ala68, 75]-Dk-(62-85).
KW Major histocompatibility complex class 1; MHC 1; cell receptor;
KW alpha 1 domain; peptide [Ala68, 75]-Dk-(62-85); interaction modulation;
KW arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PF 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 24 AA;

Query Match 86.8%; Score 46; DB 13; Length 24;
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rtllry 23
 | | | |
 QY 1 RILLY 6

RESULT 14
 ID R71436 standard; peptide; 24 AA.
 AC R71436;
 DE 12-OCT-1995 (first entry)
 DT Human MHC 1 alpha 1 domain peptide [Ala70, 77]-DK-(62-85).
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;
 KW alpha 1 domain; peptide [Ala70, 77]-DK-(62-85); interaction modulation;
 KW arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN W09505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI: 95-098577/13.
 PT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71424-R71438 are human major histocompatibility complex class 1
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
 CC were used to modulate interactions between MHC 1 and cell surface
 CC receptors. Via competitive inhibition the peptides diminish the
 CC receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.
 SQ Sequence 24 AA;

Query Match 86.8%; Score 46; DB 13; Length 24;
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rtllry 23
 | | | |
 QY 1 RILLY 6

RESULT 15
 ID R71427 standard; peptide; 24 AA.
 AC R71427;
 DE 12-OCT-1995 (first entry)
 DT Human MHC 1 alpha 1 domain peptide [Ala74]-DK-(62-85).
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;
 KW alpha 1 domain; peptide [Ala74]-DK-(62-85); interaction modulation;
 KW arthritis; neoplasias; lupus erythematosus.
 OS Homo sapiens.
 PN W09505189-A.
 PD 23-FEB-1995.
 PF 12-AUG-1994; U09189.
 PR 12-AUG-1993; US-105416.
 PA (REGC) UNIV CALIFORNIA.
 PI Goldstein A, Goodenow RS, Olsson L;
 DR WPI: 95-098577/13.
 PT Regulating cell surface receptor response - by modulating
 PT interaction between MHC class I antigen and the cell surface
 PT receptor
 PS Example 4; Page 45; 103pp; English.
 CC R71424-R71438 are human major histocompatibility complex class 1
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
 CC were used to modulate interactions between MHC 1 and cell surface
 CC receptors. Via competitive inhibition the peptides diminish the
 CC receptors response, this feature may be useful for the treatment
 CC of neoplasias, lupus erythematosus and arthritis.

SQ Sequence 24 AA;

Query Match 86.8%; Score 46; DB 13; Length 24;
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rtllry 23
 | | | |
 QY 1 RILLY 6

Search completed: Thu May 22 08:44:00 1997
 Job time : 9 secs.

THIS PAGE BLANK (USPTO)

MILES (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:42:00 1997; MasPar time 2.57 Seconds
66.443 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-4
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 RIALRY 6

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 2850787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 21.604; Variance 27.804; scale 0.777

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | No. | Score | Match | Length | DB | ID | Description | Pred. | No. |
|--------|-------|-----|-------|-------|--------|----|----|-------------|-------|-----|
|--------|-------|-----|-------|-------|--------|----|----|-------------|-------|-----|

No matches found.

Search completed: Thu May 22 08:42:12 1997
JOB time : 12 secs.

THIS PAGE BLANK (USPTO)

WORLD (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:41:35 1997; MasPar time 1.89 Seconds
Tabular output not generated. 67.442 Million cell updates/sec

Title: >US-08-653-294-4
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 RIALRY 6

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 22.521; Variance 22.707; scale 0.992

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

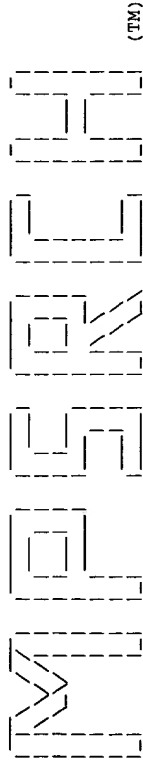
SUMMARIES

| Result | Query | % |
|--------|-------|--|
| No. | Score | Match Length DB ID Description Pred. No. |

No matches found.

Search completed: Thu May 22 08:41:43 1997
Job time : 8 secs.

THIS PAGE BLANK (USPTO)



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:42:30 1997; MasPar time 1.75 Seconds
Tabular output not generated. 37.295 Million cell updates/sec

Title: >US-08-653-294-4
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 RIALRY 6

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 15.638; Variance 39.027; scale 0.401

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|-----------------------|-----------|
| 1 | 49 | 100.0 | 10 18 | R95413 | Alpha-helix of HLA-B | 1.25e+01 |
| 2 | 49 | 100.0 | 10 18 | R95425 | HLA-B2702.75-84(D). | 1.25e+01 |
| 3 | 49 | 100.0 | 10 18 | R41208 | Peptide fragment of C | 1.25e+01 |
| 4 | 49 | 100.0 | 10 16 | R83062 | HLA-B2702 CTL modul | 1.25e+01 |
| 5 | 49 | 100.0 | 10 16 | R83094 | HLA-B2702 CTL modul | 1.25e+01 |
| 6 | 49 | 100.0 | 12 18 | R95429 | HLA-B2702 84-79-84 pa | 1.25e+01 |
| 7 | 49 | 100.0 | 15 16 | R92912 | HLA-B2702 CTL modul | 1.25e+01 |
| 8 | 49 | 100.0 | 20 18 | R95428 | HLA-B2702 84-75-84 pa | 1.25e+01 |
| 9 | 49 | 100.0 | 20 16 | R92907 | HLA-B2702 CTL modul | 1.25e+01 |
| 10 | 49 | 100.0 | 20 16 | R92908 | HLA-B2702 CTL modul | 1.25e+01 |
| 11 | 49 | 100.0 | 25 18 | R95416 | HLA-B2702.60-84. | 1.25e+01 |
| 12 | 49 | 100.0 | 25 18 | R95422 | HLA-B2702 CTL modul | 1.25e+01 |
| 13 | 49 | 100.0 | 25 16 | R83090 | HLA-B2702 CTL modul | 1.25e+01 |
| 14 | 49 | 100.0 | 25 8 | R41205 | Peptide fragment of C | 1.25e+01 |
| 15 | 49 | 100.0 | 25 16 | R83093 | HLA-B2702 CTL modul | 1.25e+01 |
| 16 | 49 | 100.0 | 25 8 | R42866 | Peptide fragment of H | 1.25e+01 |
| 17 | 45 | 91.8 | 43 18 | R92804 | PB145 serpin enzyme c | 4.07e+01 |
| 18 | 42 | 85.7 | 10 18 | R95426 | HLA-B2702.75-84(T). | 9.64e+01 |
| 19 | 42 | 85.7 | 10 16 | R83096 | HLA-B2702 CTL modul | 9.64e+01 |

20 42 85.7 10 16 R83095 HLA-B2702 CTL modul 9.64e+01
21 42 85.7 20 16 R92910 HLA-B2702 CTL modul 9.64e+01
22 42 85.7 20 16 R92909 HLA-B2702 CTL modul 9.64e+01

Note: Post-processor removed 23 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1

ID R95413 standard; peptide; 10 AA.
AC R95413;
DT 12-NOV-1996 (first entry)
DE Alpha-helix of HLA-B2702.
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example: Page 11; 29pp; English.
CC This sequence represents the alpha-helix of the
CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,
CC epitopes, and palindromes of it (such as R95428) can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition the
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.25e+01; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Db 5 rialry 10
QY 1 RIALRY 6

RESULT 2

ID R95425 standard; peptide; 10 AA.
AC R95425;
DT 12-NOV-1996 (first entry)
DE HLA-B2702.75-84(D).
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN Key Location/Qualifiers
FH Misc.difference 3
FT /note= "N3D mutation"

PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT compns. comprising lymphoid surface membrane proteins - which may
 PS inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702.75-84(D). These sequences can be used to isolate the protein
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs) by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 CC Sequence 10 AA;

Query Match 100.0%; Score 49; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10
 |||||
 QY 1 RIALRY 6

RESULT 3
 ID R41208 standard; peptide; 10 AA.
 AC R41208;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN W09317699-A.
 PD 16-SEP-1993.
 PF 23-FEB-1993; U01758.
 PR 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI; 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 11; Page 54; 61pp; English.
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
 CC activity, either by inhibition or stimulation. It can be used
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 CC This peptide sequence is more commonly found within larger peptide
 CC compounds of not more than 30 amino acids in length.
 CC Sequence 10 AA;

Query Match 100.0%; Score 49; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10
 |||||
 QY 1 RIALRY 6

RESULT 4
 ID R83062 standard; peptide; 10 AA.
 AC R83062;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; Graft versus host disorder; transplantation; therapy;
 KW Class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Claim 15; Page 9; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC Class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the Class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 10 AA;

Query Match 100.0%; Score 49; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10
 |||||
 QY 1 RIALRY 6

RESULT 5
 ID R83094 standard; peptide; 10 AA.
 AC R83094;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; Graft versus host disorder; transplantation; therapy;
 KW Class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 14; Page 34; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC Class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the Class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with

CC a subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10
 |||||
 QY 1 RIALRY 6

RESULT 6
 ID R95429 standard; peptide; 12 AA.

AC R95429;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-79-84 palindromic.
 KW HLA: p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; UL2985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-79-84 palindromic. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.

Query Match 100.0%; Score 49; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 rialry 12
 |||||
 QY 1 RIALRY 6

RESULT 7

ID R92912 standard; peptide; 15 AA.
 AC R92912;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.70-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/45.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 15 AA;

Query Match 100.0%; Score 49; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 rialry 15
 |||||
 QY 1 RIALRY 6

RESULT 8

ID R95428 standard; peptide; 20 AA.
 AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75-84 palindromic.
 KW HLA: p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; UL2985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75-84 palindromic. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 15 r1aly 20
 QY 1 RIALRY 6
 |||||

RESULT 9
 ID R92907 standard; peptide; 20 AA.
 AC R92907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 15 r1aly 20
 QY 1 RIALRY 6
 |||||

RESULT 10
 ID R92908 standard; peptide; 20 AA.
 AC R92908;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 15 r1aly 20
 QY 1 RIALRY 6
 |||||

RESULT 11
 ID R95416 standard; peptide; 25 AA.
 AC R95416;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702.60-84.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents
 CC HLA-B2702.60-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC this sequence, induces calcium influx, and inhibits cytotoxic T
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can
 CC be screened for their effect on the cytolytic activity of T-cells, by
 CC combining them with the extracellular portion of p74 and determining the
 CC amount of binding between the candidate compound and p74. Modulation of
 CC CTL activity can be inhibited in a cellular composition containing
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the
 CC extracellular portion of p74, in an amount sufficient to compete with p74
 CC for the binding of the p74 ligand.
 CC Sequence 25 AA;

Query Match 100.0%; Score 49; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 20 r1aly 25
 |||||

QY 1 RIALRY 6

RESULT 12
ID R95422 standard; peptide; 25 AA.

AC R95422;

DT 12-NOV-1996 (first entry)

DE HLAB38.6084.

KW HLA; p74: alpha1-helix; human-leucocyte-associated antigen; inhibitor;

KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;

KW cytolysis; antigen presenting cell.

OS Synthetic.

PN W09513288-A1.

PD 18-MAY-1995.

PF 10-NOV-1994; U12985.

PR 10-NOV-1993; US-150493.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM;

DR WPI; 95-194027/25.

PT Compsns. comprising lymphoid surface membrane proteins - which may

PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 9; 25pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC a T-cell lysate. p74 is a T-cell surface membrane protein associated
CC with T-cell activation in mammalian T-cells, and is also immunologically
CC cross reactive with the heat shock protein Hsc70. p74 is found in a
CC limited number of cell types, but is particularly expressed on B and T
CC cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B2702 palindromic peptide.

CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.

SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 18; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25

|||||

QY 1 RIALRY 6

RESULT 13

ID R83090 standard; peptide; 25 AA.

AC R83090;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.60-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Farham P;

DR WPI; 95-358562/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R82907-R82913 represent fragments of
CC Class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with
CC a subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 16; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25

|||||

QY 1 RIALRY 6

RESULT 14

ID R41205 standard; peptide; 25 AA.

AC R41205;

DT 15-MAR-1994 (first entry)

DE Peptide fragment of Class I HLA peptide.

KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;

KW parasitic disease; cytotoxic T lymphocyte; modulation.

OS Synthetic.

PN W09317699-A.

PD 16-SEP-1993.

PF 25-FEB-1993; U01758.

PR 02-MAR-1992; US-844716.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger CA, Krensky AM;

DR WPI; 93-303134/38.

PT New peptide(s) based on Class I HLA antigen domains - used for

PT modulating cytotoxic T-lymphocyte activity towards targets

PS Claim 8; Page 53; 61pp; English.

CC The peptide (or a fragment of at least 10 amino acids, joined at at

CC least one terminus to a sequence other than that of wild type HLA

CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,

CC either by inhibition or stimulation. It can be used for

CC inhibiting CTL toxicity in transplantations, for inducing CTL

CC activity in parasitic diseases and neoplasia and in studies on viral

CC infection. The peptide can also be used for identifying CTLs which

CC bind to it and removing subsets of CTLs from a T-cell composition.

SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 8; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25

|||||

QY 1 RIALRY 6

RESULT 15

ID R83093 standard; peptide; 25 AA.

AC R83093;

DT 16-MAY-1996 (first entry)

DE HLAB38 CTL modulating peptide (B38.6084).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLAB38.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Kremsky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 13; Page 32; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLAB38. These sequences can be used to extend the period of acceptance
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides
 CC are administered to a patient in conjunction with a subtherapeutic amount
 CC of an immunosuppressant. This is administered to the patient for a
 CC limited period of time (compared to the lifetime administration for
 CC current treatments). The peptides particularly modulate (or inhibit) the
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 r1alry 25
 |||||
 QY 1 RIALRY 6

Search completed: Thu May 22 08:42:40 1997
 Job time : 10 secs.

MPERCH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:44:44 1997; MasPar time 2.46 Seconds
69.444 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-6
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 YRLLIR 6

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 22.841; Variance 31.665; scale 0.721

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------------|--------|-------|-------------|-----------|
| ----- | | | | | |

No matches found.

Search completed: Thu May 22 08:44:53 1997
Job time: 9 secs.

THIS PAGE BLANK (USPTO)

Db 232 yslirrkplfy 243
| | | | |
QY 1 YRLAIRIALRY 12

RESULT 13
ID RUB2_BRANA STANDARD; PRT; 583 AA.
AC P34794;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD
CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA).
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALE; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94302182.
RA COLE K.P., BLAKELEY S.D., DENNIS D.T.;
RL PLANT PHYSIOL. 105:453-453(1994).
CC -!- FUNCTION: THIS PROTEIN BINDS RUBISCO SMALL AND LARGE SUBUNITS AND
IS IMPLICATED IN THE ASSEMBLY OF THE ENZYME OLIGOMER.
CC -!- SUBUNIT: OLIGOMER OF PROBABLY SIX ALPHA AND SIX BETA SUBUNITS.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- THIS PROTEIN SHOWS ATPASE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; 227222; G415925; -.
DR PIR; S38642; S38642.
DR PROSITE; PS00296; CHAPERONINS_CPN60.
DR CHAPERONE; ATP-BINDING; CHLOROPLAST; TRANSIT PEPTIDE.
KW CHAPERONE; ATP-BINDING; CHLOROPLAST (BY SIMILARITY).
FT TRANSIT 1 45 CHLOROPLAST
FT CHAIN 46 583 RUBISCO SUBUNIT BINDING-PROTEIN ALPHA.
SQ SEQUENCE 583 AA; 61605 MW; 44188FDD CRC32;

Query Match 56.1%; Score 55; DB 9; Length 583;
Best Local Similarity 63.6%; Pred. No. 1.17e+01;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 34 yrkanrfrslr 44
| | | | |
QY 1 YRLAIRIALRY 11

RESULT 14
ID DNL4_HUMAN STANDARD; PRT; 844 AA.
AC P49917;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DNA LIGASE IV (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)).
GN LIG4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=PROSTATE;
RX MEDLINE; 95280920.
RA WEI Y.-F., ROBINS P., CARTER K., CALDECOTT K., PAPPIN D.J.C.,
RA YU G.-L., WANG R.-P., SHELL B.K., NASH R.A., SCHAR P., BARNES D.E.,
RA HASELTINE W.A., LINDAHL T.;
RL MOL. CELL. BIOL. 15:3206-3216(1995).
CC -!- CATALYTIC ACTIVITY: ATP + (DEOXYRIBONUCLEOTIDE)(N) +
(DEOXYRIBONUCLEOTIDE)(M) -> AMP + PYROPHOSPHATE +
(DEOXYRIBONUCLEOTIDE)(N+M).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- TISSUE SPECIFICITY: TESTIS, THYMUS, PROSTATE AND HEART.
CC -!- SIMILARITY: HIGH TO OTHER EUKARYOTIC AND VIRUSES DNA LIGASES, LOW
TO PHAGES LIGASES.
DR EMBL; X83441; G860937; -.
KW DNA REPAIR; DNA REPLICATION; DNA RECOMBINATION; CELL DIVISION; LIGASE;

KW ATP-BINDING; NUCLEAR PROTEIN.
FT BINDING 206 206 AMP (BY SIMILARITY).
SQ SEQUENCE 844 AA; 96154 MW; A4C8599F CRC32;

Query Match 56.1%; Score 55; DB 3; Length 844;
Best Local Similarity 54.5%; Pred. No. 1.17e+01;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 770 rlaikalelrf 780
| | | | |
QY 2 RLAIIRIALRY 12

RESULT 15
ID APOA_MACMU STANDARD; PRT; 1420 AA.
AC P14417;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE APOLIPOPROTEIN(A) (EC 3.4.21.-) (APO(A)) (LP(A)) (FRAGMENT).
GN LPA.
OS MACACA MULATTA (RHESUS MACAQUE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89174660.
RA TOMLINSON J.E., MCLEAN J.W., LAWN R.M.;
RL J. BIOL. CHEM. 264:5957-5965(1989).
CC -!- FUNCTION: APO(A) IS THE MAIN CONSTITUENT OF LIPOPROTEIN(A). APO(A)
CAN BIND TO FIBRONECTIN AND HAS SERINE PROTEINASE ACTIVITY CAPABLE
OF CLEAVING IT.
CC -!- SUBUNIT: APO(A) IS DISULFIDE LINKED TO APO-B100.
CC -!- DISEASE: CONCENTRATION OF LP(A) IN PLASMA IS CORRELATED WITH
ATHEROSCLEROSIS.
CC -!- SIMILARITY: CONTAINS FOUR KRINGLE REGIONS.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY. BELONGS TO THE PLASMINOGEN SUBFAMILY.
DR EMBL; J04635; G342073; -.
DR PIR; A30848; A30848.
DR PIR; A32869; A32869.
DR HSP; P00766; 1CHG.
DR PROSITE; PS00021; KRINGLE.
DR PROSITE; PS00134; TRYPSIN_HIS.
DR PROSITE; PS00135; TRYPSIN_SER.
KW HYDROLASE; SERINE PROTEASE; LIPID TRANSPORT; PLASMA; GLYCOPROTEIN;
KW KRINGLE; DUPLICATION; REPEAT; ATHEROSCLEROSIS.
SQ SEQUENCE 1420 AA; 158367 MW; 03F1D517 CRC32;

Query Match 56.1%; Score 55; DB 1; Length 1420;
Best Local Similarity 85.7%; Pred. No. 1.17e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 873 rriply 879
| | | | |
QY 6 RLAIIRY 12

Search completed: Thu May 22 08:36:00 1997
Job time : 8 secs.

```

QY      1 YRLAIRRIALRY 12
      ||| |:::
RESULT  10
ID YCD4_YEAST      STANDARD;      PRT;      212 AA.
AC P25369;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 23.6 KD PROTEIN IN GLK1-STES5 INTERGENIC REGION.
GN YCL34W OR YCL186.
OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMICETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91377317.
RA RAD M.R., LUTZENKIRCHEN K., XU G., KLEINHANS U., HOLLENBERG C.P.;
RL YEAST 7:533-538(1991).
DR EMBL; X59720; E264423; -.
DR PIR; S19362; S19362.
DR PIR; S17476; S17476.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 212 AA; 23590 MW; 35F0A90E CRC32;

Query Match      56.1%; Score 55; DB 11; Length 212;
Best Local Similarity 77.8%; Pred.No. 1.17e+01;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 115 alrrkvlry 123
      |||| |
QY      4 AIRRIALRY 12

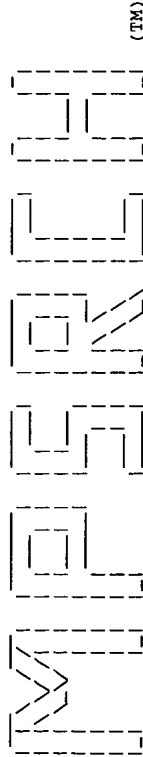
RESULT  11
ID ACHE_BOVIN      STANDARD;      PRT;      491 AA.
AC P02715;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON CHAIN PRECURSOR.
GN CHRNE.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85240565.
RA TAKAI T., NODA M., MISHINA M., SHIMIZU S., FURUTANI Y., KAYANO T.,
RA IKEDA T., KUBO T., TAKAHASHI H., TAKAHASHI T., KUNO M., NUMA S.;
RL NATURE 315:761-764(1985).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC MUSCLE) CHAINS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85240565.
RA TAKAI T., NODA M., MISHINA M., SHIMIZU S., FURUTANI Y., KAYANO T.,
RA IKEDA T., KUBO T., TAKAHASHI H., TAKAHASHI T., KUNO M., NUMA S.;
RL NATURE 315:761-764(1985).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC MUSCLE) CHAINS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC EMBL; X02597; G57; -.
DR PIR; A03174; ACBOE.
DR PROSITE; PS00236; NEUOTR_ION_CHANNEL.
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
KW TRANSMEMBRANE.
FT SIGNAL 1 20
FT CHAIN 21 491 ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON.
FT DOMAIN 21 239 EXTRACELLULAR.
FT TRANSMEM 240 264
FT DOMAIN 265 272 CYTOPLASMIC.
FT TRANSMEM 273 291
FT DOMAIN 292 306 EXTRACELLULAR.
FT TRANSMEM 307 328
FT DOMAIN 329 456 CYTOPLASMIC.
FT TRANSMEM 457 480
FT DOMAIN 481 493 EXTRACELLULAR.
FT DISULFID 148 162 BY SIMILARITY.
FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 161 161 PROBABLE.
SQ SEQUENCE 493 AA; 54697 MW; 2BA86189 CRC32;

Query Match      56.1%; Score 55; DB 1; Length 493;
Best Local Similarity 58.3%; Pred.No. 1.17e+01;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 YRLAIRRIALRY 12
      ||| |:::
RESULT  12
ID ACHE_HUMAN      STANDARD;      PRT;      493 AA.
AC Q04844;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON CHAIN PRECURSOR.
GN CHRNE OR ACHRE.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-MUSCLE FIBROBLAST;
RX MEDLINE; 93345508.
RA BEESON D.M.W., BRIDSON M., BETTY M., JEREMIAH S., POVEY S.,
RA VINCENT A., NEWSOM-DAVIS J.;
RL EUR. J. BIOCHEM. 215:229-238(1993).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC MUSCLE) CHAINS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC EMBL; X66403; G560153; -.
DR PIR; S29601; S29601.
DR PIR; S34775; S34775.
DR MM; 100725; -.
DR PROSITE; PS00236; NEUOTR_ION_CHANNEL.
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
KW TRANSMEMBRANE; PHOSPHORYLATION.
FT SIGNAL 1 20
FT CHAIN 21 493 ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON.
FT DOMAIN 21 239 EXTRACELLULAR.
FT TRANSMEM 240 264
FT DOMAIN 265 272 CYTOPLASMIC.
FT TRANSMEM 273 291
FT DOMAIN 292 306 EXTRACELLULAR.
FT TRANSMEM 307 328
FT DOMAIN 329 456 CYTOPLASMIC.
FT TRANSMEM 457 480
FT DOMAIN 481 493 EXTRACELLULAR.
FT DISULFID 148 162 BY SIMILARITY.
FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 161 161 PROBABLE.
SQ SEQUENCE 493 AA; 54697 MW; 2BA86189 CRC32;

Query Match      56.1%; Score 55; DB 1; Length 493;
Best Local Similarity 58.3%; Pred.No. 1.17e+01;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```



Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:44:16 1997; MasPar time 1.84 Seconds
69.215 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-6
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 YRLJIR 6

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 23.777; Variance 26.124; scale 0.910

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

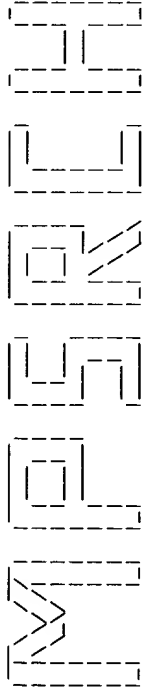
SUMMARIES

| Result | Query | % |
|--------|-------|--|
| No. | Score | Match Length DB ID Description Pred. No. |

No matches found.

Search completed: Thu May 22 08:44:25 1997
Job time : 9 secs.

THIS PAGE BLANK (COPY)



Release 2.1D John F. Collins, BioComputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:46:31 1997; MasPar time 1.77 Seconds
Tabular output not generated. 36.872 Million cell updates/sec

Title: >US-08-653-294-7
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 YRLAIR 6

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 15.681; Variance 40.195; scale 0.390

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|-----------------------|-----------|
| 1 | 49 | 100.0 | 12 18 | R95429 | HLA-B2702 84-79-84 pa | 1.52e+01 |
| 2 | 49 | 100.0 | 20 18 | R95430 | HLA-B2702 84-75T/75-8 | 1.52e+01 |
| 3 | 49 | 100.0 | 20 18 | R95428 | HLA-B2702 84-75-84 pa | 1.52e+01 |
| 4 | 49 | 100.0 | 20 16 | R92909 | HLA-B2702 CTL modul | 1.52e+01 |
| 5 | 49 | 100.0 | 20 16 | R92911 | HLA-B2702 CTL modul | 1.52e+01 |
| 6 | 49 | 100.0 | 20 16 | R92907 | HLA-B2702 CTL modul | 1.52e+01 |
| 7 | 45 | 91.8 | 43 11 | R58902 | Drosophila-12 cadher | 4.80e+01 |
| 8 | 45 | 91.8 | 43 17 | R87142 | Protocadherin clone D | 4.80e+01 |
| 9 | 42 | 85.7 | 20 16 | R92910 | HLA-B2702 CTL modul | 1.11e+02 |
| 10 | 42 | 85.7 | 20 16 | R92908 | HLA-B2702 CTL modul | 1.11e+02 |

Note: Post-processor removed 35 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID R95429 standard; peptide; 12 AA.
AC R95429;

DT 12-NOV-1996 (first entry)
DE HLA-B2702 84-79-84 palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
PS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PT (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702 84-79-84 palindrome. These sequences can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 12 AA;

Query Match 100.0%; Score 49; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.52e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
Qy 1 YRLAIR 6

RESULT 2
ID R95430 standard; peptide; 20 AA.
AC R95430;
DT 12-NOV-1996 (first entry)
DE HLA-B2702 84-75T/75-84T palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
PS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PT (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702 84-75T/75-84T palindrome. These sequences can be used to
CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
CC membrane protein associated with T-cell activation in mammalian T-cells,

CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B2702 60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.
 CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 CC Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
 |||||
 QY 1 YRLAIR 6

RESULT 3
 ID R95428 standard; peptide; 20 AA.

AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75-84 palindromic.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.

PF 18-MAY-1995.
 PD 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.

PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75-84 palindromic. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702 60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 CC Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6

QY 1 YRLAIR 6
 |||||

RESULT 4

ID R92909 standard; peptide; 20 AA.
 AC R92909;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.

PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
 |||||
 QY 1 YRLAIR 6

RESULT 5

ID R92911 standard; peptide; 20 AA.
 AC R92911;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.

PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
 |||||
 QY 1 YRLAIR 6

RESULT 6

ID R2907 standard; peptide; 20 AA.
 AC R2907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW Class I MHC; HLA-B*2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R83907-R83914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
 |||||
 QY 1 YRLAIR 6

RESULT 7

ID R58902 standard; Protein; 43 AA.
 AC R58902;
 DT 17-APR-1995 (first entry)
 DE Drosophila-12 cadherin-related molecule.
 KW Cadherin; cell adhesion molecule.
 OS Drosophila.
 PN W09414960-A.
 PD 07-JUL-1994.
 PF 23-DEC-1993; U12588.
 PR 29-DEC-1992; US-998003.
 PA (DOHE-) DOHENY EYE INST.
 PI Suzuki S;
 DR WPI; 94-293849/36.
 DR N-PSDB; Q68993.
 PT Polynucleotide sequences encoding new proto:cadherins - useful
 for modulating natural binding and regulating activities.
 Example; Page 63; 114pp; English.
 CC Two regions of conserved AA sequence, one from the middle of the
 CC third cadherin extracellular subdomain (EC-3) and the other from the
 CC C-terminus of the fourth extracellular subdomain (EC-4) were
 CC identified. The corresp. degenerate oligos (Q68949, Q68950) were
 CC designed for use as PCR primers. PCR was carried out on a rat brain
 CC cDNA prep. Two major bands of about 450 bps and 130 bps were found.
 CC The 450 bp band corresponded to the expected length between the two
 CC primer sites, but the 130 bp band could not be predicted from any
 CC of the previously identified cadherin sequences. The 450 bp and 130
 CC bp bands were extracted and sequenced. Nineteen novel partial cDNA
 CC clones were isolated. The DNA and deduced AA sequences of the
 CC clones (including sequences corresp. to the PCR primers) are given
 CC in Q68951-Q68969 and R58860-R58878. Various cDNA fragments
 CC structurally similar to the rat cDNAs were isolated from human,
 CC mouse and Xenopus brain cDNA preps. and from Drosophila and
 CC C. elegans whole body cDNA preps. by PCR using the above primers.
 CC The DNA and deduced AA sequences of the resulting PCR fragments
 CC (including sequences corresp. to the PCR primers) are given in
 CC Q68971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison
 CC of the deduced AA sequences indicates a similarity, in particular,
 CC there are three sets of clones that appear to be cross-species
 CC homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and
 CC HUMAN-11; and MOUSE-326 and HUMAN-42.
 SQ Sequence 43 AA;

Query Match 91.8%; Score 45; DB 11; Length 43;
 Best Local Similarity 83.3%; Pred. No. 4.80e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 yrlvir 16
 |||||
 QY 1 YRLAIR 6

RESULT 8

ID R87142 standard; Peptide; 43 AA.
 AC R87142;
 DT 29-AUG-1996 (first entry)
 DE Protocadherin clone DROSOPHILA-12.
 KW Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse;
 KW catenin; therapy; clone; frog; fruit fly.
 OS Drosophila melanogaster.
 FH Key Location/Qualifiers
 FT Misc_difference 38
 FT /note= "encoded by CGA"
 FT Misc_difference 39
 FT /note= "encoded by ATG"
 FT Misc_difference 40
 FT /note= "encoded by ACA"
 FT Misc_difference 41
 FT /note= "encoded by ATG"
 FT Misc_difference 42
 FT /note= "encoded by CGC"
 FT Misc_difference 43
 FT /note= "encoded by CGC"
 PN W09600289-A1.
 PD 04-JAN-1996.
 PR 26-JUN-1995; U08071.
 PR 27-JUN-1994; US-268161.
 PA (DOHE-) DOHENY EYE INST.
 PI Suzuki S;
 DR WPI; 96-068873/07.
 DR N-PSDB; T03617.
 PT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat
 PT pc5 - involved in cell-cell adhesion and regulation activities
 PS Example 2; Page 67-68; 146pp; English.
 CC R87142-R87144 represent partial fragments of the drosophila protocadherin
 CC sequence. The cDNAs encoding these sequences were isolated after
 CC screening a drosophila whole body cDNA preparation with the primers shown
 CC in T03575 and T03576. The primers were constructed from portions of the
 CC amino acid sequences of the third and fourth extracellular domains of

CC published cadherin sequences. The cytoplasmic domain of cadherin
 CC interacts with the cytoskeleton through catenins and other cytoskeleton
 CC associated proteins. The cytoplasmic domain is not present in all
 CC cadherins, but in those which possess it, it is essential for the
 CC cadherins adhesive function. The cadherins which do not possess a
 CC cytoplasmic domain appear to function via a different method from those
 CC with a cytoplasmic domain. These protein sequences are involved in
 CC cell-cell adhesion. These sequences may have regulatory functions in the
 CC cell, as well as the cell-cell adhesive properties. Antibodies produced
 CC against these sequences are useful for modulating the binding activity of
 CC these protocadherins, and can be used therapeutically.
 SQ Sequence 43 AA;

Query Match 91.8%; Score 45; DB 17; Length 43;

Best Local Similarity 83.3%; Pred. No. 4.80e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 yrlvir 16

QY 1 YRLAIR 6

RESULT 9

ID R92910 standard; peptide; 20 AA.

AC R92910;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).

DW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PI (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

SQ Sequence 20 AA;

Query Match 85.7%; Score 42; DB 16; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.11e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlvir 6

QY 1 YRLAIR 6

RESULT 10

ID R92908 standard; peptide; 20 AA.

AC R92908;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).

DW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PI (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

SQ Sequence 20 AA;

Query Match 85.7%; Score 42; DB 16; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.11e+02;

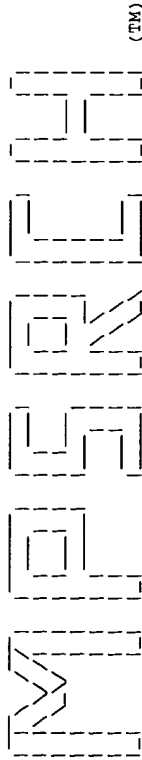
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlvir 6

QY 1 YRLAIR 6

Search completed: Thu May 22 08:46:40 1997

Job time : 9 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:46:03 1997; MasPar time 2.50 Seconds
Tabular output not generated. 68.363 Million cell updates/sec

Title: >US-08-653-294-7
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 YRLAIR 6

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 21.577; Variance 27.148; scale 0.795

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | | | | |
|--------|-------|-------|--------|----|-------------|
| No. | Score | Match | Length | ID | Description |
| | | | | | Pred. No. |

No matches found.

Search completed: Thu May 22 08:46:13 1997
Job time : 10 secs.

THIS PAGE BLANK (USPTO)

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
 Distribution rights by Intelligenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:32:13 1997; MasPar time 1.92 Seconds
 Tabular output not generated. 33.977 Million cell updates/sec

Title: >US-08-653-294-7
 Description: (1-6) from US08653294.pep
 Perfect score: 49
 Sequence: 1 YRLAIR 6

Scoring table:
 GAP 150
 PAM 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq26
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19

Statistics: Mean 15.681; Variance 40.195; scale 0.390

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|------------------------|
| 1 | 49 | 100.0 | 12 | 18 | R95429 | HLA-B2702 84-79-84 pa |
| 2 | 49 | 100.0 | 20 | 18 | R95430 | HLA-B2702 84-75T/75-8 |
| 3 | 49 | 100.0 | 20 | 18 | R95428 | HLA-B2702 84-75-84 pa |
| 4 | 49 | 100.0 | 20 | 16 | R32909 | HLA-B2702 CTL modul |
| 5 | 49 | 100.0 | 20 | 16 | R32911 | HLA-B2702 CTL modul |
| 6 | 49 | 100.0 | 20 | 16 | R32907 | HLA-B2702 CTL modul |
| 7 | 45 | 91.8 | 43 | 11 | R38902 | Drosophila-12 cadher |
| 8 | 45 | 91.8 | 43 | 17 | R87142 | Protocadherin clone D |
| 9 | 44 | 89.8 | 724 | 18 | R33081 | Bacillus thuringiensis |
| 10 | 44 | 89.8 | 772 | 15 | R79949 | Enzyme M-11. |
| 11 | 44 | 89.8 | 775 | 15 | R79950 | Enzyme Q36. |
| 12 | 42 | 85.7 | 20 | 16 | R32910 | HLA-B2702 CTL modul |
| 13 | 42 | 85.7 | 20 | 16 | R32908 | HLA-B2702 CTL modul |
| 14 | 41 | 83.7 | 617 | 8 | R42392 | McI haemagglutinin. |
| 15 | 41 | 83.7 | 732 | 2 | R11056 | Acylamino acid-isolat |
| 16 | 41 | 83.7 | 732 | 3 | R20001 | Human acyl amino acid |
| 17 | 41 | 83.7 | 783 | 13 | R70841 | E. coli polymerase-II |
| 18 | 41 | 83.7 | 783 | 5 | R24441 | E. coli DNA polymeras |
| 19 | 41 | 83.7 | 783 | 1 | P34265 | Sequence of APH36.1 c |
| 20 | 40 | 81.6 | 232 | 1 | P80760 | Deduced peptide seque |

| 21 | 40 | 81.6 | 248 | 3 | P60437 | Dog 32 kd alveolar su |
|----|----|------|------|----|--------|------------------------|
| 22 | 40 | 81.6 | 256 | 1 | R04210 | Canine 32K alveolar s |
| 23 | 40 | 81.6 | 855 | 6 | R29815 | S receptor kinase pro |
| 24 | 40 | 81.6 | 896 | 1 | R05551 | The 36 kd antigen of |
| 25 | 40 | 81.6 | 1157 | 9 | R48678 | Insecticidal protoxin |
| 26 | 40 | 81.6 | 1288 | 3 | R20073 | N-methylhydantoinase. |
| 27 | 40 | 81.6 | 1528 | 18 | R95333 | Manduca sexta Bacillu |
| 28 | 39 | 79.6 | 635 | 14 | R75940 | Human myeloproliferat |
| 29 | 39 | 79.6 | 635 | 4 | R23970 | MPLV env protein with |
| 30 | 39 | 79.6 | 643 | 18 | R97735 | Bacillus thuringiensis |
| 31 | 39 | 79.6 | 643 | 1 | P91462 | 67-kD protein toxin. |
| 32 | 39 | 79.6 | 816 | 12 | R58564 | Retinoblastoma 94kd t |
| 33 | 39 | 79.6 | 816 | 11 | R58568 | Human retinoblastoma |
| 34 | 39 | 79.6 | 816 | 1 | P82112 | Human retinoblastoma |
| 35 | 39 | 79.6 | 928 | 1 | R05305 | Cancer supressing gen |
| 36 | 39 | 79.6 | 928 | 13 | R71680 | Retinoblastoma ppl10R |
| 37 | 39 | 79.6 | 928 | 14 | R74271 | Retinoblastoma tumour |
| 38 | 39 | 79.6 | 928 | 1 | R06289 | Predicted retinoblast |
| 39 | 39 | 79.6 | 928 | 7 | R36534 | Retinoblastoma (RB) p |
| 40 | 39 | 79.6 | 928 | 13 | R71681 | Retinoblastoma (RB) p |
| 41 | 39 | 79.6 | 970 | 1 | P90599 | Human retinoblastoma. |
| 42 | 39 | 79.6 | 1723 | 19 | W00645 | Mouse DEC-205. |
| 43 | 39 | 79.6 | 1743 | 19 | W00644 | Human DEC-205. |
| 44 | 39 | 79.6 | 3398 | 8 | R44430 | eryA region polypepti |
| 45 | 38 | 77.6 | 341 | 19 | W02699 | G-protein coupled hum |

ALIGNMENTS

RESULT 1
 ID R95429 standard; peptide; 12 AA.
 AC R95429;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-79-84 palindrome.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM,
 DR WPI; 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-79-84 palindrome. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 49; DB 18; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;

| | |
|--|---|
| PI | Clayberger C, Krensky AM; |
| DR | WPI; 95-194027/25. |
| PT | Compns. comprising lymphoid surface membrane proteins - which may |
| PS | Inhibit cytolytic activity and differentiation of CTLs. |
| PE | Example: Page 12; 29pp; English. |
| CC | R95413, and R95415-R95431 represent palindromes and fragments of |
| CC | human-leucocyte-associated antigens. This sequence represents the |
| CC | HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate |
| CC | the protein p74 from a T-cell lysate. p74 is a T-cell surface membrae |
| CC | protein associated with T-cell activation in mammalian T-cells, and is |
| CC | also immunologically cross reactive with the heat shock protein Hsc70. |
| CC | p74 is found in a limited number of cell types, but is particularly |
| CC | expressed on B and T cells. p74 can be isolated by lysis of a suitable |
| CC | cell with an amphoteric detergent, and then passed through an affinity |
| CC | column containing a covalently bound HLA-B2702 palindromic peptide. |
| CC | Compositions comprising the extracellular fragment of p74 combined with |
| CC | HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits |
| CC | cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate |
| CC | compounds can be screened for their effect on the cytolytic activity of |
| CC | T-cells, by combining them with the extracellular portion of p74 and |
| CC | determining the amount of binding between the candidate compound and p74 |
| CC | Modulation of CTL activity can be inhibited in a cellular composition |
| CC | containing T-cells and antigen presenting cells (APCs), by adding to the |
| CC | mix the extracellular portion of p74, in an amount sufficient to compete |
| CC | with p74 for the binding of the p74 ligand. |
| CC | Sequence 20 AA; |
| SQ | |
| | |
| Query Match 100.0%; Score 49; DB 18; Length 20; | |
| Best Local Similarity 100.0%; Pred. No. 1.52e+01; | |
| Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| | |
| Db | 1 Yrlair 6 |
| QY | 1 YRLAIR 6 |
| | |
| RESULT | 4 |
| ID | R92909 standard; peptide; 20 AA. |
| AC | R92909; |
| AD | 16-MAY-1996 (first entry) |
| DE | HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)). |
| KW | Cytotoxic T Lymphocyte; CTL; major histocompatibility complex; MHC; |
| KW | Immunosuppressant; graft versus host disorder; transplantation; therapy; |
| KW | Class I MHC; HLA-B2702. |
| OS | Synthetic. |
| PN | WO9526979-A1. |
| PD | 12-OCT-1995. |
| PF | 05-APR-1995; PF U04349. |
| PR | 05-APR-1994; US-222851. |
| PA | (STRD) UNIV LELAND STANFORD JUNIOR. |
| PI | Clayberger C, Krensky AM, Parham P; |
| PT | WPI; 95-358582/46. |
| PT | Extension of acceptance period of transplants from MHC unmatched |
| PT | donor hosts - using Class I B75-84 MHC antigen of the recipient |
| PT | host |
| PS | Example 15; Page 36; 80pp; English. |
| CC | R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of |
| CC | Class I major histocompatibility complex (MHC) antigens. This sequence |
| CC | is an inverted dimer of residues 75-84 of the alpha-1 domain of the class |
| CC | I MHC HLA-B2702. These sequences can be used to extend the period of |
| CC | acceptance by a recipient of a transplant from an MHC unmatched donor. |
| CC | The peptides are administered to a patient in conjunction with a |
| CC | subtherapeutic amount of an immunosuppressant. This is administered to |
| CC | the patient for a limited period of time (compared to the lifetime |
| CC | administration for current treatments). The peptides particularly |
| CC | modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) |
| CC | of the patient. |
| CC | Sequence 20 AA; |
| SQ | |
| | |
| Query Match 100.0%; Score 49; DB 16; Length 20; | |
| Best Local Similarity 100.0%; Pred. No. 1.52e+01; | |
| Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |

Db 1 yrlair 6
QY 1 YRLAIR 6

RESULT 5
ID R92911 standard; peptide: 20 AA.
AC R92911;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.52e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
QY 1 YRLAIR 6

RESULT 6
ID R92907 standard; peptide: 20 AA.
AC R92907;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a

subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.52e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6
QY 1 YRLAIR 6

RESULT 7
ID R58902 standard; Protein; 43 AA.
AC R58902;
DT 17-APR-1995 (first entry)
DE Drosophila-12 cadherin-related molecule.
KW Cadherin; cell adhesion molecule.
OS Drosophila.
PN W09414960-A.
PD 07-JUL-1994.
PF 23-DEC-1993; U12588.
PR 29-DEC-1992; US-998003.
PA (DOHE-) DOHENY EYE INST.
PI Suzuki S;
DR WPI: 94-293849/36.
DR N-PSDB; 068993.
PT Polynucleotide sequences encoding new proto-cadherins - useful for modulating natural binding and regulating activities.
PS Example; Page 63; 14pp; English.
CC Two regions of conserved AA sequence, one from the middle of the third cadherin extracellular subdomain (EC-3) and the other from the C-terminus of the fourth extracellular subdomain (EC-4) were identified. The corresp. degenerate oligos (Q68949, Q68950) were designed for use as PCR primers. PCR was carried out on a rat brain cDNA prep. Two major bands of about 450 bps and 130 bps were found. The 450 bp band corresponded to the expected length between the two primer sites, but the 130 bp band could not be predicted from any of the previously identified cadherin sequences. The 450 bp and 130 bp bands were extracted and sequenced. Nineteen novel partial cDNA clones were isolated. The DNA and deduced AA sequences of the clones (including sequences corresp. to the PCR primers) are given in Q68951-Q68969 and R58860-R58878. Various cDNA fragments structurally similar to the rat cDNAs were isolated from human, mouse and xenopus brain cDNA preps. and from Drosophila and C. elegans whole body cDNA preps. by PCR using the above primers. The DNA and deduced AA sequences of the resulting PCR fragments (including sequences corresp. to the PCR primers) are given in Q68971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison of the deduced AA sequences indicates a similarity, in particular, there are three sets of clones that appear to be cross-species homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and HUMAN-11; and MOUSE-326 and HUMAN-42.
SQ Sequence 43 AA;

Query Match 91.8%; Score 45; DB 11; Length 43;
Best Local Similarity 83.3%; Pred. No. 4.80e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 yrlvir 16
QY 1 YRLAIR 6

RESULT 8
ID R87142 standard; Peptide; 43 AA.
AC R87142;
DT 29-AUG-1996 (first entry)
DE Protocadherin clone DROSOPHILA-12.

| | |
|-----|---|
| KW | Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse; |
| OS | catenin; therapy; clone; frog; fruit fly. |
| KS | Drosophila melanogaster. |
| Key | Location/Qualifiers |
| FT | Misc_difference 38 |
| FT | /note= "encoded by CGA" |
| FT | Misc_difference 39 |
| FT | /note= "encoded by ATG" |
| FT | Misc_difference 40 |
| FT | /note= "encoded by ACA" |
| FT | Misc_difference 41 |
| FT | /note= "encoded by ATG" |
| FT | Misc_difference 42 |
| FT | /note= "encoded by CGC" |
| FT | Misc_difference 43 |
| FT | /note= "encoded by CGC" |
| PN | W09600289-A1. |
| PD | 04-JAN-1996. |
| PE | 26-JUN-1995; U08071. |
| PR | 27-JUN-1994; US-268161. |
| PA | (DOHE-) DOHENY EYE INST. |
| PI | Suzuki S; |
| DI | WPI: 96-068873/07. |
| DR | N-PSDB: T03617. |
| PT | Poly nucleotide(s) encoding human protocadherins pc3 and pc4 and rat |
| PT | pc5 - involved in cell-cell adhesion and regulation activities |
| PS | Example 2; page 67-68; 146pp; English. |
| CC | R87142-R87144 represent partial fragments of the drosophila protocadherin |
| CC | sequence. The cDNAs encoding these sequences were isolated after |
| CC | screening a drosophila whole body cDNA preparation with the primers shown |
| CC | in T03575 and T03576. The primers were constructed from portions of the |
| CC | amino acid sequences of the third and fourth extracellular domains of |
| CC | published cadherin sequences. The cytoplasmic domain of cadherin |
| CC | interacts with the cytoskeleton through catenins and other cytoskeleton |
| CC | associated proteins. The cytoplasmic domain is not present in all |
| CC | cadherins, but in those which possess it, it is essential for the |
| CC | cadherins adhesive function. The cadherins which do not possess a |
| CC | cytoplasmic domain appear to function via a different method from those |
| CC | with a cytoplasmic domain. These protein sequences are involved in |
| CC | cell-cell adhesion. These sequences may have regulatory functions in the |
| CC | cell, as well as the cell-cell adhesive properties. Antibodies produced |
| CC | against these sequences are useful for modulating the binding activity of |
| CC | these protocadherins, and can be used therapeutically. |
| SQ | Sequence 43 AA; |

```

Query Match          91.8%; Score 45; DB 17; Length 43;
Best Local Similarity 83.3%; Pred. NO. 4.80e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      11 yrlvir 16
      ||| ||
      1 YRLAIR 6

Query 1 YRLAIR 6

RESULT 9
ID      R93081 standard; Protein; 724 AA.
AC      R93081;
DT      04-OCT-1996 (first entry)
DE      Bacillus thuringiensis insecticidal protein JEG80.
KW      Insecticidal crystal toxin; jeg80; anti-diptera; mosquito; larvae;
KW      Aedes aegypti; Anopheles stephensi; Culex pipiens; Atjcg 367.
OS      Bacillus thuringiensis ser. jegathesan 367.
PN      W09506171-A2.
PD      29-FEB-1996.
PF      24-AUG-1995; F01116.
PR      25-AUG-1994; FR-010299.
PI      (INSP ) INST PASTEUR.
PI      Delecluse A, Thierly I;
DR      WPI: 96-151374/15.
DR      N-PSDB: T17044.
PT      New B.thuringiensis ser. jegathesan insecticidal proteins - and
PT      related DNA, with high activity against dipteran larvae, e.g.
PT      A.aegypti, A.stephensi or C.pipiens

```

PS Clalm 17; Fig 5; 55pp; French.

CC The present sequence is that of the JEG80 protein which was isolated

CC from *Bacillus thuringiensis* ser. jegathesan 367 (BTjeg367); it is

CC a crystal toxin of mol. wt. 80 kD which is active against dipteran

CC insects, esp. mosquitoes. The full-length, recombinant JEG80 toxin,

CC had mean LC50 values (in ng/ml) after 48 hours of 18.8, 42.7 and

CC 10.1 against larvae of *Aedes aegypti*, *Anopheles stephensi* and *Culex*

CC pipiens, respectively. Wild-type Btjeg367 crystals gave values of

CC 47.4, 54.5 and 9.6. The JEG80 protein is far more toxic (6-40 times

CC more toxic against the mosquito species tested) than the Bt cryIID

CC toxin, despite their close sequence similarity.

CC Sequence 724 AA;

Query Match 89.8%; Score 44; DB 18; Length 724;
Best Local Similarity 83.3%; Pred. No. 6.37e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 548 yrlir 553
||| ||

QY 1 YRLAIR 6

RESULT 10

ID R79949 standard; Protein; 772 AA.

AC R79949;

DT 24-APR-1996 (first entry)

DE Enzyme M-11.

KW Enzyme; M-11; Q36; rhizobium; arthrobacter; trehalose;
amylaceous saccharide.

OS Rhizobium sp. M11.

FS Key Location/Qualifiers

FT Misc_difference 502..506

FT /note= "used for production of probe sequence (T04206) "

FT Misc_difference 621..625

FT /note= "used for production of probe sequence (T04207) "

PN EP-674005-K2.

PD 27-SEP-1995.

PF 23-FEB-1995; 301176.

PR 23-FEB-1994; JP-047956.

PR 23-FEB-1994; JP-047940.

PR 06-APR-1994; JP-090728.

PR 06-APR-1994; JP-090705.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Kubota M, Maruta K, Sugimoto T, Tsusaki K;
WPI; 95-329870/43.

DR N-PSDB; T04155.

DR DNA encoding enzyme reduces amylaceous saccharide to produce
non-reducing sugar with trehalose end gp. - useful in foods,
PT cosmetics, pharmaceuticals, etc.

PT

PS Clalm 3; Page 21-22; 178pp; English.

CC This sequence represents an enzyme that forms a non-reducing sugar with a
CC trehalose end group, from a reducing amylaceous saccharide. The

CC amylaceous saccharides have a degree of glucose polymerisation of 3 or
CC higher. This sequence was extracted from a liquid culture of *Rhizobium*

CC species M-11. By using an oligonucleotide probe based on a fragment of
CC this sequence, the encoding sequence was obtained. The encoding sequence
CC was then ligated into a vector and used to produce M-11 in *E.coli*

CC transformants. This can also be performed for the DNA encoding enzyme
CC Q36 (see T04156), which was obtained from *Arthrobacter* sp. Q36. The
CC non-reducing sugars produced by the action of these enzymes can be used
CC in foods, cosmetics, pharmaceuticals and feeds. They are used as
CC sweeteners, taste and quality improvers, stabilisers, fillers, excipients
CC and adjuvants. The sugars can also be used as intermediates for
CC trehalose. The advantages with using these sugars, are that, they are
CC practically non-reducing (so no browning reaction occurs when they are
CC heated with proteins), have a mild but good quality sweetness, adequate
CC viscosity and moisture-retaining properties.

CC Sequence 772 AA;

SQ

```
Query Match      89.8%; Score 44; DB 15; Length 772;
Best Local Similarity 83.3%; Pred. No. 6.37e+01;
Matches      5; Conservative      0; Mismatches 1; Indels 0; Gaps 0;
```

```

Db      8 Yrlqir 13
QY      1 YRLAIR 6

RESULT 11
ID R79950 standard; Protein; 775 AA.
AC R79950;
DT 24-APR-1996 (first entry)
DE Enzyme Q36.
KW Enzyme; M-11; Q36; rhizobium; arthrobacter; trehalose;
   amylose saccharide.
OS Arthrobacter sp. M11.
FH Key Location/Qualifiers
FT Misc difference 120..125
FT /note= "used for production of probe sequence (T04209)"
FT Misc difference 621..625
FT /note= "used for production of probe sequence (T04210)"
PN EP-674005-A2.
PD 27-SEP-1995.
PF 23-FEB-1995; 301176.
PR 23-FEB-1994; JP-047956.
PR 23-FEB-1994; JP-047940.
PR 06-APR-1994; JP-090728.
PR 06-APR-1994; JP-090705.
PA (HAYE ) HAYASHIBARA SEIBUTSU KAGAKU.
PI Kubota M, Maruta K, Sugimoto T, Tsusaki K;
DR WPI: 95-329870/43.
DR N-PSDB: T04156.
PT DNA encoding enzyme reduces amylaceous saccharide to produce
   non-reducing sugar with trehalose end gp. - useful in foods,
   cosmetics, pharmaceuticals, etc.
PS Claim 3; Page 23-25; 178pp; English.
CC This sequence represents an enzyme that forms a non-reducing sugar with a
   trehalose end group, from a reducing amylose saccharide. The
   amylose saccharides have a degree of glucose polymerisation of 3 or
   higher. This sequence was extracted from a liquid culture of
   Arthrobacter species Q36. By using an oligonucleotide probe based on a
   fragment of the enzyme sequence, the DNA encoding sequence was obtained.
   The encoding sequence was then ligated into a vector and used to produce
   M-11 in E.coli transformants. This can also be performed for the DNA
   encoding enzyme M-11 (see T04155), which was obtained from Rhizobium sp.
   M-11. The non-reducing sugars produced by the action of these enzymes
   can be used in foods, cosmetics, pharmaceuticals and feeds. They are
   used as sweeteners, taste and quality improvers, stabilisers, fillers,
   excipients and adjuvants. The sugars can also be used as intermediates
   for trehalose. The advantages with using these sugars, are that, they
   are practically non-reducing (so no browning reaction occurs when they
   are heated with proteins), have a mild but good quality sweetness,
   adequate viscosity and moisture-retaining properties.
SQ Sequence 775 AA;

Query Match      89.8%; Score 44; DB 15; Length 775;
Best Local Similarity 83.3%; Pred. No. 6.37e-01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      8 Yrlqir 13
QY      1 YRLAIR 6

RESULT 12
ID R92910 standard; peptide; 20 AA.
AC R92910;
DT 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
   immunosuppressant; graft versus host disorder; transplantation; therapy;
   class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
   immunosuppressant; graft versus host disorder; transplantation; therapy;
   class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.

Query Match      89.8%; Score 44; DB 15; Length 775;
Best Local Similarity 83.3%; Pred. No. 6.37e-01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      8 Yrlqir 13
QY      1 YRLAIR 6

RESULT 13
ID R92908 standard; peptide; 20 AA.
AC R92908;
DT 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
   immunosuppressant; graft versus host disorder; transplantation; therapy;
   class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
   donor hosts - using Class I B75-84 MHC antigen of the recipient
   host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
   class I major histocompatibility complex (MHC) antigens. This sequence
   is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
   I MHC HLA-B*2702. These sequences can be used to extend the period of
   acceptance by a recipient of a transplant from an MHC unmatched donor.
   The peptides are administered to a patient in conjunction with a
   subtherapeutic amount of an immunosuppressant. This is administered to
   the patient for a limited period of time (compared to the lifetime
   administration for current treatments). The peptides particularly
   modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
   of the patient.
SQ Sequence 20 AA;

Query Match      85.7%; Score 42; DB 16; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.11e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      1 Yrlatr 6
QY      1 YRLAIR 6

Query Match      85.7%; Score 42; DB 16; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.11e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      1 Yrlatr 6
QY      1 YRLAIR 6

RESULT 14

```

ID R42392 standard; Protein; 617 AA.
AC R42392;
DT 13-MAY-1994 (first entry)
DE MCI haemagglutinin.
KW Haemagglutinin; HA; fusion glycoprotein; wild-type;
KW measles virus; vaccine; infection; consensus polypeptide.
OS Measles virus strain MCI.
PN WO9321325-A.
PD 28-OCT-1993.
PF 08-APR-1993; U03209.
PR 08-APR-1992; US-866033.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
PI Bellini WJ, Rota JS;
DR WPI: 93-351735/44.
DR N-PSDB; Q51093.
PT Haemagglutinin and fusion glycoprotein of several wild-type
PT measles strains - used to construct vaccines for measles
PT infection
PS Claim 11; Page 47-50; 119pp; English.
CC HA (Q51088-94) and fusion glycoprotein (Q51095-97) sequences of
CC several wild-type measles strains are given. Shared amino acid
CC variations in wild-type measles glycoproteins are identified in five
CC wild-type measles viruses. A consensus polypeptide, the amino acid
CC sequence of which reflects variation common to more than one wild-
CC type strain, is the basis for constructing live attenuated vaccines,
CC or recombinant vaccines to replace older, less efficacious vaccines.
CC Immunological reagents useful in differentiating wild-type measles
CC strains from other known strains can also be produced.
SQ Sequence 617 AA;

Query Match 83.7%; Score 41; DB 8; Length 617;
Best Local Similarity 66.7%; Pred. No. 1.47e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

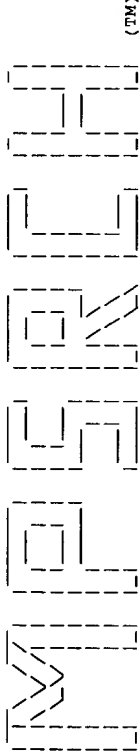
Db 555 frlpir 560
QY 1 YRLAIR 6

RESULT 15
ID R11056 standard; Protein; 732 AA.
AC R11056;
DT 23-MAY-1991 (first entry)
DE Acylamino acid-isolating enzyme-like polypeptide.
KW AARE; pig liver.
OS Sus scrofa.
PN J03030673-A.
PD 08-FEB-1991.
PF 29-JUN-1989; 165216.
PR 29-JUN-1989; JP-165216.
PA (TAKA-) TAKARA SHUZO KK.
DR WPI: 91-084340/12.
DR N-PSDB; Q10958.
PT Acylamino acid-isolating enzyme-like polypeptide - prepd. by
PT genetic engineering.
PS Claim 1; Fig 2; 10pp; Japanese.
CC The sequence was obt'd. from six clones isolated from a pig liver
CC cDNA library. The clones, lambda AARE 419, 450, 451, 452, 521 and
CC 522 cover the entire sequence of the gene.
SQ Sequence 732 AA;

Query Match 83.7%; Score 41; DB 2; Length 732;
Best Local Similarity 66.7%; Pred. No. 1.47e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 268 frlpir 273
QY 1 YRLAIR 6

Search completed: Thu May 22 08:32:26 1997
Job time : 13 secs.



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:29:29 1997; MasPar time 2.04 Seconds
Tabular output not generated. 62.314 Million cell updates/sec

Title: >US-08-653-294-6
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 YRLLR 6

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 23.777; Variance 26.124; scale 0.910

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|----------------------------------|-----------|
| 1 | 51 | 96.2 | 1489 | 11 | YGPO_YEAST HYPOTHETICAL 171.5 KD | 1.06e+00 |
| 2 | 49 | 92.5 | 101 | 11 | YEB4_YEAST HYPOTHETICAL 12.2 KD | 2.96e+00 |
| 3 | 49 | 92.5 | 720 | 6 | NDA4_SCHPO CELL DIVISION CONTROL | 2.96e+00 |
| 4 | 48 | 90.6 | 221 | 11 | YFH8_YEAST HYPOTHETICAL 25.9 KD | 4.88e+00 |
| 5 | 48 | 90.6 | 239 | 11 | YJ9D_YEAST HYPOTHETICAL 27.6 KD | 4.88e+00 |
| 6 | 48 | 90.6 | 309 | 9 | TF2B_SULSH TRANSCRIPTION INITIAT | 4.88e+00 |
| 7 | 48 | 90.6 | 628 | 4 | GIDA_BACSU GLUCOSE INHIBITED DIV | 4.88e+00 |
| 8 | 48 | 90.6 | 629 | 4 | GIDA_HAEIN GLUCOSE INHIBITED DIV | 4.88e+00 |
| 9 | 48 | 90.6 | 968 | 6 | MANA_RHOMR MANNAN ENDO-1,4-BETA- | 4.88e+00 |
| 10 | 48 | 90.6 | 1075 | 8 | RPOB_PINTH DNA-DIRECTED RNA POLY | 4.88e+00 |
| 11 | 47 | 88.7 | 1089 | 6 | NMD2_YEAST NONSENSE-MEDIATED MRN | 7.98e+00 |
| 12 | 46 | 86.8 | 234 | 7 | PRC3_DROME PROTEASOME 25 KD SUBU | 1.29e+01 |
| 13 | 46 | 86.8 | 332 | 11 | YK50_YEAST HYPOTHETICAL 39.4 KD | 1.29e+01 |
| 14 | 46 | 86.8 | 1070 | 8 | RPOB_TOBAC DNA-DIRECTED RNA POLY | 1.29e+01 |
| 15 | 46 | 86.8 | 1070 | 8 | RPOB_SPTOL DNA-DIRECTED RNA POLY | 1.29e+01 |
| 16 | 45 | 86.8 | 1078 | 8 | RPOB_SINAL DNA-DIRECTED RNA POLY | 1.29e+01 |
| 17 | 45 | 84.9 | 293 | 8 | RL5_CAEEL PROBABLE 60S RIBOSOMA | 2.08e+01 |
| 18 | 45 | 84.9 | 513 | 8 | RFP_HUMAN TRANSFORMING PROTEIN | 2.08e+01 |
| 19 | 45 | 84.9 | 1030 | 3 | FBI1_DROME FAT-BODY PROTEIN-1 PR | 2.08e+01 |
| 20 | 45 | 84.9 | 1638 | 2 | BRM_DROME HOMEOTIC GENE REGULAT | 2.08e+01 |
| 21 | 44 | 83.0 | 181 | 10 | VC16_VACCC PROTEIN C16/B22 | 3.32e+01 |
| 22 | 44 | 83.0 | 187 | 8 | RL18_ARATH 60S RIBOSOMAL PROTEIN | 3.32e+01 |

| | | | | | | |
|----|----|------|------|----|----------------------------------|----------|
| 23 | 44 | 83.0 | 233 | 7 | PRC3_XENLA PROTEASOME COMPONENT | 3.32e+01 |
| 24 | 44 | 83.0 | 258 | 11 | YDF2_SCHPO HYPOTHETICAL 29.3 KD | 3.32e+01 |
| 25 | 44 | 83.0 | 293 | 8 | RL5_SCHPO 60S RIBOSOMAL PROTEIN | 3.32e+01 |
| 26 | 44 | 83.0 | 297 | 8 | RL1_YEAST 60S RIBOSOMAL PROTEIN | 3.32e+01 |
| 27 | 44 | 83.0 | 515 | 9 | TRPE_BUCAP ANTHRANILATE SYNTHASE | 3.32e+01 |
| 28 | 44 | 83.0 | 547 | 9 | SNG1_YEAST NITROGUANADINE RESI | 3.32e+01 |
| 29 | 44 | 83.0 | 590 | 11 | YKTA_CAEEL HYPOTHETICAL 65.5 KD | 3.32e+01 |
| 30 | 44 | 83.0 | 628 | 4 | GIDA_ECOLI GLUCOSE INHIBITED DIV | 3.32e+01 |
| 31 | 44 | 83.0 | 975 | 5 | KINH_DROME KINESIN HEAVY CHAIN | 3.32e+01 |
| 32 | 44 | 83.0 | 1151 | 4 | GRI1_YEAST GRI1 PROTEIN | 3.32e+01 |
| 33 | 44 | 83.0 | 2493 | 3 | CYAA_USTMA ADENYLATE CYCLASE (EC | 3.32e+01 |
| 34 | 43 | 81.1 | 146 | 9 | SR14_YEAST SIGNAL RECOGNITION PA | 5.24e+01 |
| 35 | 43 | 81.1 | 185 | 11 | YEM4_YEAST HYPOTHETICAL 21.2 KD | 5.24e+01 |
| 36 | 43 | 81.1 | 205 | 11 | YIJC_HAEIN HYPOTHETICAL PROTEIN | 5.24e+01 |
| 37 | 43 | 81.1 | 234 | 11 | YIJC_ECOLI HYPOTHETICAL 26.6 KD | 5.24e+01 |
| 38 | 43 | 81.1 | 394 | 7 | PHYV_PSEAE P-HYDROXYBENZOATE HYD | 5.24e+01 |
| 39 | 43 | 81.1 | 394 | 7 | PHYV_PSEFL P-HYDROXYBENZOATE HYD | 5.24e+01 |
| 40 | 43 | 81.1 | 601 | 6 | LONH_HAEIN PROTEASE LA HOMOLOG (| 5.24e+01 |
| 41 | 43 | 81.1 | 779 | 11 | YX31_MYCTU HYPOTHETICAL 84.6 KD | 5.24e+01 |
| 42 | 43 | 81.1 | 825 | 8 | RCAL_YEAST MITOCHONDRIAL RESPIRA | 5.24e+01 |
| 43 | 43 | 81.1 | 1592 | 4 | GTF2_STRDO GLUCOSYLTRANSFERASE-I | 5.24e+01 |
| 44 | 43 | 81.1 | 1597 | 4 | GTF1_STRDO GLUCOSYLTRANSFERASE-I | 5.24e+01 |
| 45 | 43 | 81.1 | 4092 | 3 | DYHC_YEAST DYNEIN HEAVY CHAIN, C | 5.24e+01 |

ALIGNMENTS

RESULT 1
ID YGPO_YEAST STANDARD; PRT; 1489 AA.
AC PS3115;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE HYPOTHETICAL 171.5 KD HELICASE IN LYSS-ARO2 INTERGENIC REGION.
GN YGL150C OR G1880.
OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96158061.
RA JAMES C.M., INDGE K.J., OLIVER S.G.;
RL YEAST 11:1413-1419(1995).
RN [2]
RP SEQUENCE OF 138-1489 FROM N.A.
RA VOLCKAERT G., VOLT M., VERHASSELT P., DEFOOR E.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- SIMILARITY: TO HELICASES OF THE SNF2/RAD54 FAMILY.
DR EMBL; 248618; G728695; -.
DR EMBL; 272672; E243594; -.
KW HYPOTHETICAL PROTEIN; NUCLEAR PROTEIN; DNA-BINDING; HELICASE;
KW ATP-BINDING.
FT DOMAIN 188 193 POLY-ALA.
FT DOMAIN 259 268 POLY-GLU.
FT DOMAIN 300 306 POLY-SER.
FT DOMAIN 568 573 POLY-GLU.
FT DOMAIN 675 682 POLY-GLU.
FT NP_BIND 731 738 ATP (POTENTIAL).
FT SITE 841 844 DEAQ BOX.
SQ SEQUENCE 1489 AA; 171454 MW; 81498878 CRC32;
Query Match 96.2%; Score 51; DB 11; Length 1489;
Best Local Similarity 83.3%; Pred.No. 1.06e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1420 yrlivr 1425
QY 1 YRLLR 6
RESULT 2
ID YEB4_YEAST STANDARD; PRT; 101 AA.
AC P39399;

01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 12.2 KD PROTEIN IN MMS21-UBC8 INTERGENIC REGION.
 GN YEL014C.
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,
 RA AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.,
 RA CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICK-SMITH S.,
 RA HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,
 RA MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OENER P., OH C.,
 RA PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH V.,
 RA TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.,
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U18530; G602381; -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 101 AA; 12209 MW; BE5A484B CRC32;

Query Match 92.5%; Score 49; DB 11; Length 101;
 Best Local Similarity 83.3%; Pred. No. 2.96e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 92 ymlir 97

QY 1 YRLIR 6

RESULT 3
 ID NDA4_SCHPO STANDARD; PRT; 720 AA.
 AC P41389;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CELL DIVISION CONTROL PROTEIN NDA4.
 GN NDA4 OR SPAC3F10.01.
 OS SCHIOSACCHAROMYCES POMBE (FISSTON YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94129084.
 RA MIYAKE S., OKISHIO N., SAMEJIMA I., HIRAOKA Y., TODA T., SAITOH I.,
 RA YANAGIDA M.;
 RA MOL. BIOL. CELL 4:1003-1015(1993).
 RL [2]
 RP SEQUENCE OF 72-720 FROM N.A.
 RC STRAIN-972;
 RA MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: ROLE IN DNA REPLICATION AND ESSENTIAL FOR VIABILITY.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE MCM2/3/5 FAMILY.
 DR EMBL; S58467; G545211; -
 DR EMBL; Z69369; E221200; -
 DR PIR; A48723; A48723.
 DR PROSITE; PS00847; MCM235.
 KW TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 KW DNA REPLICATION; CELL CYCLE; ATP-BINDING.
 FT DOMAIN 307 312 POLY-GLU.
 FT DOMAIN 322 529 MCM.
 FT NP_BIND 372 379 ATP (POTENTIAL).
 FT CONFLICT 461 461 A -> R (IN REF. 1).
 SQ SEQUENCE 720 AA; 80099 MW; 29D61458 CRC32;

Query Match 92.5%; Score 49; DB 6; Length 720;
 Best Local Similarity 83.3%; Pred. No. 2.96e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 675 ymlir 680

QY 1 YRLIR 6

QY 1 YRLIR 6
 RESULT 4
 ID YFH8_YEAST STANDARD; PRT; 221 AA.
 AC P43592;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 25.9 KD PROTEIN IN MPRI-GCN20 INTERGENIC REGION.
 GN YFR008W.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RX MEDLINE; 95400292.
 RA MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,
 RA SASANUMA S.-I., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,
 RA YAMAZAKI M., TASHIRO H., EKI T.;
 RL NAT. GENET. 10:261-268(1995).
 DR EMBL; D50617; G836763; -
 KW HYPOTHETICAL PROTEIN.
 FT DOMAIN 11 22 POLY-GLN.
 SQ SEQUENCE 221 AA; 25915 MW; 3D34764A CRC32;

Query Match 90.6%; Score 48; DB 11; Length 221;
 Best Local Similarity 83.3%; Pred. No. 4.88e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 211 yrlir 216

QY 1 YRLIR 6

RESULT 5
 ID YJ9D_YEAST STANDARD; PRT; 239 AA.
 AC P47167;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 27.6 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.
 GN YJRI35C OR J2122.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ROSE M., KOETTER P., ENTIAN K.D.;
 RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; Z49635; G1015872; -
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 239 AA; 27567 MW; 0BF23C6E CRC32;

Query Match 90.6%; Score 48; DB 11; Length 239;
 Best Local Similarity 83.3%; Pred. No. 4.88e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 205 yrlir 210

QY 1 YRLIR 6

RESULT 6
 ID TF2B_SULSH STANDARD; PRT; 309 AA.
 AC P50387;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).
 GN TFB.
 OS SULFOLOBUS SHIBATAE.
 OC ARCHAEABACTERIA; CRENARCHAEOTA; SULFOLOBALES.
 RN [1]

```

RX SEQUENCE FROM N.A.
RA MEDLINE; 95320218.
RA OURESHI S.A., KHOO B., BAUMANN P., JACKSON S.P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 92:6077-6081(1995).
CC -!- SIMILARITY: BELONGS TO THE IFIB FAMILY.
DR EMBL; U20899; G836952; -.
KW TRANSCRIPTION REGULATION; DUPLICATION.
FT REPEAT 130 206
FT REPEAT 224 300
SQ SEQUENCE 309 AA; 34756 MW; 0921E52C CRC32;

Query Match          90.6%; Score 48; DB 9; Length 309;
Best Local Similarity 83.3%; Pred. No. 4.88e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 201 yrl1lr 206
QY 1 YRL1LR 6

RESULT 7
ID GIDA_BACSU STANDARD; PRT; 628 AA.
AC P25812;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GLUCOSE INHIBITED DIVISION PROTEIN A.
GN GIDA.
OS BACILLUS SUBTILIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / CRK2000;
RX MEDLINE; 92204018.
RA OGASAWARA N., YOSHIKAWA H.;
RL MOL. MICROBIOL. 6:629-634(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE; 96051385.
RA OGASAWARA N., NAKAI S., YOSHIKAWA H.;
RL DNA RES. 1:11-14(1994).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: TO OTHER BACTERIAL GIDA PROTEIN.
DR EMBL; X62539; G40026; -.
DR EMBL; D26185; G467385; -.
DR PIR; JQ1216; EWSGA.
DR SUBTILIST; BG10059; GIDA.
SQ SEQUENCE 628 AA; 69752 MW; F9B082BB CRC32;

Query Match          90.6%; Score 48; DB 4; Length 628;
Best Local Similarity 83.3%; Pred. No. 4.88e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 435 yrl1lr 440
QY 1 YRL1LR 6

RESULT 8
ID GIDA_HAEIN STANDARD; PRT; 629 AA.
AC P44763;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GLUCOSE INHIBITED DIVISION PROTEIN A.
GN GIDA OR HI0582.
OS HAEMOPHILUS INFLUENZAE.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;

```

```

RX MEDLINE; 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
RA UTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.; 496-512(1995).
RL SCIENCE 269:496-512(1995).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: TO OTHER BACTERIAL GIDA PROTEIN.
DR EMBL; I45233; G1004046; -.
DR EMBL; U32739; G925610; -.
SQ SEQUENCE 629 AA; 70103 MW; 6FD83D06 CRC32;

Query Match          90.6%; Score 48; DB 4; Length 629;
Best Local Similarity 83.3%; Pred. No. 4.88e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 435 yrl1lr 440
QY 1 YRL1LR 6

RESULT 9
ID MANA_RHOMR STANDARD; PRT; 968 AA.
AC P49425;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MANNAN ENDO-1,4-BETA-MANNOSIDASE (EC 3.2.1.78).
GN MANA.
OS RHODOTHERMUS MARINUS.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
OC NONPHOTOSYNTHETIC, NONFRUITING GLIDING; CYTOPHAGACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RA POLITZ O., KRAH M., BORRIESS R.;
RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-BETA-D-
CC LINKAGES IN MANNANS, GALACTOMANNANS, GLUCOMANNANS, AND
CC GALACTOGLUCOMANNANS.
CC -!- SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES.
DR EMBL; X90947; G975706; -.
KW HYDROLASE; GLYCOSIDASE.
SQ SEQUENCE 968 AA; 110219 MW; 0EA79E71 CRC32;

Query Match          90.6%; Score 48; DB 6; Length 968;
Best Local Similarity 83.3%; Pred. No. 4.88e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 692 yrl1lr 697
QY 1 YRL1LR 6

RESULT 10
ID RPOB_PINTH STANDARD; PRT; 1075 AA.
AC P41607;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
GN RPOB.
OS PINUS THUNBERGII (GREEN PINE) (JAPANESE BLACK PINE).
OC CHLOROPLAST.
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; CONIFEROPHYCEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95024047.
RA WAKASUGI T., TSUDZUKI J., ITO S., NAKASHIMA K., TSUDZUKI T.,

```

RA SUGIURA M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:9794-9798(1994).
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
 CC RNA(N).
 CC -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
 CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
 CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
 DR EMBL: D17510; GI262609; -.
 KW TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.
 SQ SEQUENCE 1075 AA; 122470 MW; 7643B7A8 CRC32;

Query Match 90.6%; Score 48; DB 8; Length 1075;
 Best Local Similarity 83.3%; Pred. No. 4.88e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1044 frllir 1049
 QY 1 YRLIIR 6
 :|||||

RESULT 11
 ID NMD2-YEAST STANDARD; PRT; 1089 AA.
 AC P38798;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE NONSENSE-MEDIATED MRNA DECAY PROTEIN 2 (UP-FRAMESHIFT SUPPRESSOR 2).
 GN NMD2 OR UPF2 OR IF51 OR SUAL OR YHRO77C.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE; 95189083.
 CC HE F., JACOBSON A.;
 CC GENES DEV. 9:437-454(1995).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN-FLY136;
 CC MEDLINE; 95189082.
 CC CUI Y., HAGAN K.W., ZHANG S., PELTZ S.W.;
 CC GENES DEV. 9:423-436(1995).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC MEDLINE; 95327692.
 CC LEE S.I., UMEN J.G., VARMUS H.E.;
 CC PROC. NATL. ACAD. SCI. U.S.A. 92:6587-6591(1995).
 CC [4]
 CC SEQUENCE FROM N.A.
 CC STRAIN-S288C / AB972;
 CC MEDLINE; 94378003.
 CC JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
 CC DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,
 CC KUCABA T., HILLIER L., JTER M., JOHNSTON L., LANGSTON Y.,
 CC LATRELLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,
 CC NATHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
 CC VIGNATI D., WILCOX L., WOLDMAN P., WATERSTON R., WILSON R.,
 CC VAUDIN M.;
 CC SCIENCE 265:2077-2082(1994).
 CC -!- FUNCTION: INVOLVED IN NONSENSE-MEDIATED DECAY OF MRNAS CONTAINING
 CC PREMATURE STOP CODONS. IT INTERACTS, VIA ITS C-TERMINUS, WITH
 CC NAM7/UPF1. COULD BE INVOLVED IN DETERMINING THE EFFICIENCY OF
 CC TRANSLATIONAL TERMINATION OR REINITIATION OR FACTORS INVOLVED IN
 CC THE INITIAL ASSEMBLY OF AN INITIATION- AND TERMINATION- COMPETENT
 CC MRNP.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC EMBL: U14974; G555939; -.
 CC ENBL: U12137; G806704; -.
 CC ENBL: U28158; G967213; -.
 CC ENBL: U10556; G500836; -.
 CC PIR: S46815; S46815.

DR SGD; L0001257; NMD2.
 FT DOMAIN 843 975 ASP/GLU-RICH (HIGHLY ACIDIC).
 ET CONFLICT 2 2 D -> YQ (IN REF. 3 AND 4).
 SQ SEQUENCE 1089 AA; 126746 MW; 4B6ADE8F CRC32;

Query Match 88.7%; Score 47; DB 6; Length 1089;
 Best Local Similarity 83.3%; Pred. No. 7.98e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 580 yrllir 585
 QY 1 YRLIIR 6
 :|||||

RESULT 12
 ID PRC3-DROME STANDARD; PRT; 234 AA.
 AC P40301;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE PROTEASOME 25 KD SUBUNIT (EC 3.4.99.46) (MULTICATALYTIC ENDOPEPTIDASE
 DE COMPLEX 25 KD SUBUNIT).
 GN PROS-25.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-CANTON-S;
 CC MEDLINE; 93363644.
 CC SEELIG A., TROXELL M., KLOETZEL P.M.;
 CC BIOCHIM. BIOPHYS. ACTA 1174:215-217(1993).
 CC -!- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
 CC NEUTRAL OR SLIGHTLY BASIC PH.
 CC -!- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL
 CC PROTEOLYTIC PATHWAY.
 CC -!- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
 CC -!- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
 CC ALSO IN THE NUCLEUS.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C3 SUBFAMILY.
 DR EMBL: X70304; G397850; -.
 DR PIR: S36116; S36116
 DR FLYBASE; FBGN0010405; PROS25.
 DR PROSITE; PS00388; PROTEASOME_A.
 KW PROTEASOME; HYDROLASE; PROTEASE.
 SQ SEQUENCE 234 AA; 25906 MW; A86BD836 CRC32;

Query Match 86.8%; Score 46; DB 7; Length 234;
 Best Local Similarity 66.7%; Pred. No. 1.29e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 83 yrllvk 88
 QY 1 YRLIIR 6
 :|||||

RESULT 13
 ID YK50-YEAST STANDARD; PRT; 352 AA.
 AC P36151;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 39.4 KD PROTEIN IN CCP1-SIS2 INTERGENIC REGION.
 GN YKR070W.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC FOHL T.M., FOHL F.M.;
 CC SUBMITTED (MAR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; Z28295; G486541; -.
 DR PIR; S38147; S38147.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 352 AA; 39406 MW; F5B1B2A CRC32;

Query Match 86.8%; Score 46; DB 11; Length 352;
 Best Local Similarity 66.7%; Pred. No. 1.29e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 223 frllvr 228
 :|||:|
 Qy 1 YRLLIR 6

RESULT 14

ID RPOB_TOBAC STANDARD; PRT; 1070 AA.
 AC P08271;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
 GN RPOB.
 OS NICOTIANA TABACUM (COMMON TOBACCO).
 OG CHLOROPLAST.
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 OC SOLANALES; SOLANACEAE.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. BRIGHT YELLOW 4;
 RA SUGIURA M.;
 RL SUBMITTED (AUG-1986) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. BRIGHT YELLOW 4;
 RX MEDLINE; 86192857.
 RA OHME M., TANAKA M., CHUNWONGSE J., SHINOZAKI K., SUGIURA M.;
 RL FEBS LETT. 200:87-90(1986).
 RN (3)
 RP COMPLETE GENOME.

RA SHINOZAKI K., OHME M., TANAKA M., WAKASUGI T., HAYASHIDA N.,
 RA MATSUBAYASHI T., ZAITA N., CHUNWONGSE J., OBOKATA J.,
 RA YAMAGUCHI-SHINOZAKI K., OHTO C., TORAZAWA K., MENG B.Y., SUGITA M.,
 RA DENO H., KAMOGASHIRA T., YAMADA K., KUSUDA J., TAKAIWA F., KATO A.,
 RA TOHDOH N., SHIMADA H., SUGIURA M.;
 RL EMBO J. 5:2043-2049(1986).
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
 RNA(N).
 CC -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
 SUBUNITS: ALPHA, BETA, BETA', AND BETA".
 CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
 DR EMBL; Z00044; G11822; -.
 DR EMBL; X12745; G11781; -.
 DR EMBL; M28017; G552958; -.
 DR PIR; A24865; RNNTB
 KW TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.
 SQ SEQUENCE 1070 AA; 120547 MW; 08C4DF19 CRC32;

Query Match 86.8%; Score 46; DB 8; Length 1070;
 Best Local Similarity 66.7%; Pred. No. 1.29e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1039 frllvr 1044
 :|||:|
 Qy 1 YRLLIR 6

RESULT 15

ID RPOB_SPIOI STANDARD; PRT; 1070 AA.
 AC P11703;
 DT 01-OCT-1989 (REL. 12, CREATED)

DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
 GN RPOB.
 OS SPINACIA OLERACEA (SPINACH).
 OG CHLOROPLAST.
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 OC CARYOPHYLLALES; CHENOPODIACEAE.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88316931.
 RA HUDSON G.S., HOLTON T.A., WHITFIELD P.R., BOTTOMLEY W.;
 RL J. MOL. BIOL. 200:639-654(1988).
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
 RNA(N).
 CC -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
 SUBUNITS: ALPHA, BETA, BETA', AND BETA".
 CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
 DR EMBL; M55297; G295121; -.
 DR PIR; C29959; C29959.
 KW TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.
 SQ SEQUENCE 1070 AA; 120899 MW; CDC6F442 CRC32;

Query Match 86.8%; Score 46; DB 8; Length 1070;
 Best Local Similarity 66.7%; Pred. No. 1.29e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1039 frllvr 1044
 :|||:|
 Qy 1 YRLLIR 6

Search completed: Thu May 22 08:29:41 1997
 Job time : 12 secs.

THIS PAGE BLANK (USPTO)

MPSRCH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:42:58 1997; MasPar time 2.50 Seconds
Tabular output not generated. 68.327 Million cell updates/sec

Title: >US-08-653-294-5
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 RILRY 6

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 22.859; Variance 32.635; scale 0.700

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | Score | Match | Length | DB ID | Description | Pred. No. |
|--------|-------|-------|-------|--------|-------|-------------|-----------|
|--------|-------|-------|-------|--------|-------|-------------|-----------|

No matches found.

Search completed: Thu May 22 08:43:09 1997
Job time : 11 secs.

THIS PAGE BLANK (USPTO)

WATERMAN (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:43:26 1997; MasPar time 1.79 Seconds
71.236 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-5
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 RILLY 6

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 23.812; Variance 26.364; scale 0.903

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | | | | |
|-----------|-------|-------|--------|----|-------------|
| No. | Score | Match | Length | ID | Description |
| Pred. No. | | | | | |

No matches found.

Search completed: Thu May 22 08:43:33 1997
Job time : 7 secs.

THIS PAGE BLANK (USPTO)

MISSREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:29:58 1997; MasPar time 2.69 Seconds
Tabular output not generated. 63.585 Million cell updates/sec

Title: >US-08-653-294-6
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 YRLIR 6

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann16:unrev

Statistics: Mean 22.841; Variance 31.665; scale 0.721

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description | Pred. No. |
|------------|-------|---------------|--------|----|-----------------------------|-----------|
| 1 | 51 | 96.2 | 1489 | 11 | S60416 DNA helicase YGL150c | 5.56e+00 |
| 2 | 49 | 92.5 | 101 | 11 | S50445 hypothetical protein | 1.30e+01 |
| 3 | 49 | 92.5 | 720 | 11 | A48723 cell division contro | 1.30e+01 |
| 4 | 48 | 90.6 | 173 | 9 | S27599 hypothetical protein | 1.97e+01 |
| 5 | 48 | 90.6 | 221 | 11 | S56263 hypothetical protein | 1.97e+01 |
| 6 | 48 | 90.6 | 239 | 11 | S57158 hypothetical protein | 1.97e+01 |
| 7 | 48 | 90.6 | 389 | 10 | JC4001 macrolide 3-O-acyl | 1.97e+01 |
| 8 | 48 | 90.6 | 628 | 4 | BWBSGA gida protein - Bacil | 1.97e+01 |
| 9 | 48 | 90.6 | 629 | 8 | I64078 glucose inhibited di | 1.97e+01 |
| 10 | 47 | 88.7 | 1089 | 11 | S48244 NMD2 protein - yeast | 2.97e+01 |
| 11 | 46 | 86.8 | 234 | 5 | S36116 multicatalytic endop | 4.45e+01 |
| 12 | 46 | 86.8 | 352 | 11 | S38147 hypothetical protein | 4.45e+01 |
| 13 | 46 | 86.8 | 1070 | 5 | C29959 DNA-directed RNA pol | 4.45e+01 |
| 14 | 46 | 86.8 | 1070 | 1 | RNNTP DNA-directed RNA pol | 4.45e+01 |
| 15 | 46 | 86.8 | 1078 | 5 | S48842 finger protein rfp - | 6.63e+01 |
| 16 | 45 | 84.9 | 506 | 6 | S37583 transforming protein | 6.63e+01 |
| 17 | 45 | 84.9 | 513 | 2 | TVHURE transforming protein | 6.63e+01 |
| 18 | 45 | 84.9 | 801 | 15 | TVHURE transforming protein | 6.63e+01 |
| 19 | 45 | 84.9 | 1030 | 12 | SVI034 gene P1 protein - fr | 6.63e+01 |
| 20 | 45 | 84.9 | 1638 | 12 | A42091 transcriptional acti | 6.63e+01 |
| 21 | 44 | 83.0 | 96 | 8 | S40544 hypothetical protein | 9.80e+01 |

| | | | | | | | |
|----|----|------|------|----|---------|----------------------|----------|
| 22 | 44 | 83.0 | 96 | 4 | IERCEE9 | hypothetical 11k pro | 9.80e+01 |
| 23 | 44 | 83.0 | 153 | 8 | A36837 | DilL protein - vaci | 9.80e+01 |
| 24 | 44 | 83.0 | 181 | 8 | C42528 | B2R protein - vari | 9.80e+01 |
| 25 | 44 | 83.0 | 234 | 5 | JH0421 | proteasome chain XC3 | 9.80e+01 |
| 26 | 44 | 83.0 | 297 | 7 | S42144 | ribosomal protein L5 | 9.80e+01 |
| 27 | 44 | 83.0 | 322 | 12 | S66766 | probable membrane pr | 9.80e+01 |
| 28 | 44 | 83.0 | 355 | 10 | I40819 | butyrate kinase - Cl | 9.80e+01 |
| 29 | 44 | 83.0 | 515 | 2 | I40052 | anthranilate synthas | 9.80e+01 |
| 30 | 44 | 83.0 | 547 | 12 | S53920 | SNG1 protein - yeast | 9.80e+01 |
| 31 | 44 | 83.0 | 590 | 12 | S40707 | hypothetical protein | 9.80e+01 |
| 32 | 44 | 83.0 | 628 | 4 | BVECOA | gida protein - Esche | 9.80e+01 |
| 33 | 44 | 83.0 | 975 | 3 | A31497 | kinesin heavy chain | 9.80e+01 |
| 34 | 44 | 83.0 | 1151 | 11 | A41529 | GRR1 protein - yeast | 9.80e+01 |
| 35 | 44 | 83.0 | 2493 | 12 | A55481 | adenylate cyclase (E | 9.80e+01 |
| 36 | 43 | 81.1 | 146 | 12 | S51616 | signal recognition p | 1.44e+02 |
| 37 | 43 | 81.1 | 158 | 4 | W6WL18 | E6 protein - human p | 1.44e+02 |
| 38 | 43 | 81.1 | 294 | 11 | S19226 | colg-regulated prote | 1.44e+02 |
| 39 | 43 | 81.1 | 363 | 12 | S59337 | RRN5 protein - yeast | 1.44e+02 |
| 40 | 43 | 81.1 | 394 | 1 | WHP5BA | 4-hydroxybenzoate 3- | 1.44e+02 |
| 41 | 43 | 81.1 | 416 | 16 | S26836 | type II site-specifi | 1.44e+02 |
| 42 | 43 | 81.1 | 505 | 10 | C64502 | hypothetical protein | 1.44e+02 |
| 43 | 43 | 81.1 | 556 | 14 | A49579 | amphotropic murine r | 1.44e+02 |
| 44 | 43 | 81.1 | 870 | 11 | S65158 | PAL1 protein - yeast | 1.44e+02 |
| 45 | 43 | 81.1 | 2148 | 14 | A56011 | transcription factor | 1.44e+02 |

ALIGNMENTS

| | | | |
|---|-------------------|---|----------------|
| 1 | RESULT | S60416 | #type complete |
| | ENTRY | DNA helicase YGL150c - yeast (Saccharomyces cerevisiae) | |
| | TITLE | protein G1880 | |
| | ALTERNATE_NAMES | #formal_name Saccharomyces cerevisiae | |
| | ORGANISM | 15-Feb-1995 #sequence_revision 12-Apr-1996 #text_change | |
| | DATE | 19-Jul-1996 | |
| | ACCESSIONS | S60416; S53049; S60421; S64166; S64164 | |
| | REFERENCE | S60416 | |
| | #authors | James, C.M.; Indge, K.J.; Oliver, S.G. | |
| | #submission | submitted to the EMBL Data Library, March 1995 | |
| | #description | DNA sequence analysis of a 35kb segment from Saccharomyces cerevisiae chromosome VII reveals 19 open reading frames including RAD54, ACE1/CUP2, PMR1, RCK1, AMS1 and CAL1/CDC43. | |
| | #accession | S60416 | |
| | #molecule_type | DNA | |
| | #residues | 1-1489 #label JAM | |
| | #cross-references | EMBL:Z48618 | |
| | REFERENCE | S53045 | |
| | #authors | James, C.M.; Indge, K.J.; Oliver, S.G. | |
| | #submission | submitted to the EMBL Data Library, March 1995 | |
| | #description | DNA sequence analysis of a 35Kb segment from S.cerevisiae chromosome VII reveals 39 ORFs including RAD54, ACE1(CUP2), PMR1, RCK1, AMS1 and CAL1/CDC43. | |
| | #accession | S53049 | |
| | #molecule_type | DNA | |
| | #residues | 816-1489 #label JAW | |
| | #cross-references | EMBL:Z48618 | |
| | REFERENCE | S60417 | |
| | #authors | James, C.M.; Indge, K.J.; Oliver, S.G. | |
| | #journal | Yeast (1995) 11:1413-1419 | |
| | #title | DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromosome VII reveals 19 open reading frames including RAD54, ACE1/CUP2, PMR1, RCK1, AMS1 and CAL1/CDC43. | |
| | #accession | S60421 | |
| | #status | nucleic acid sequence not shown | |
| | #molecule_type | DNA | |
| | #residues | 728-767;808-862;865-969;1001-1021;1296-1347;1360-1468 | |
| | #cross-references | EMBL:Z48618 | |
| | REFERENCE | S64165 | |
| | #authors | James, C.M.; Indge, K.J.; Oliver, S.G. | |
| | #submission | submitted to the Protein Sequence Database, May 1996 | |

```

#accession S64166
##molecule_type DNA
##residues 1-1489 ##label JAA
##cross-references EMBL:Z72672
##experimental_source strain S288C
REFERENCE S64153
#authors Volckaert, G.; Voet, M.; Verhasselt, P.; Defoor, E.
#submission submitted to the Protein Sequence Database, May 1996
#accession S64164
##molecule_type DNA
##residues 1-137 ##label VOL
##cross-references EMBL:Z72672
##experimental_source strain S288C
GENETICS
#map_position 7L
SUMMARY #length 1489 #molecular-weight 171454 #checksum 2554

Query Match 96.2%; Score 51; DB 11; Length 1489;
Best Local Similarity 83.3%; Pred. No. 5.56e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1420 yrllvr 1425
|||||
QY 1 YRLLIR 6

RESULT 2
ENTRY S50445 #type complete
TITLE hypothetical protein YEL014c - yeast (Saccharomyces cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 24-Feb-1995
ACCESSIONS S50445
REFERENCE S50428
#authors Dietrich, F.S.
#submission submitted to the EMBL Data Library, December 1994
#description Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 and lambda clones 6693 and 5898.
#accession S50445
##molecule_type DNA
##residues 1-101 ##label DIE
##cross-references EMBL:U18530
GENETICS
#map_position 5L
SUMMARY #length 101 #molecular-weight 12209 #checksum 4508

Query Match 92.5%; Score 49; DB 11; Length 101;
Best Local Similarity 83.3%; Pred. No. 1.30e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 92 yrmlir 97
|||||
QY 1 YRLLIR 6

RESULT 3
ENTRY A48723 #type complete
TITLE cell division control protein nda4 - fission yeast (Schizosaccharomyces pombe)
ORGANISM #formal_name Schizosaccharomyces pombe
DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 04-Dec-1994
ACCESSIONS A48723
REFERENCE A48723
#authors Miyake, S.; Okishio, N.; Samejima, I.; Hiraoka, Y.; Toda, T.; Saitoh, I.; Yanagida, M.
#journal Mol. Biol. Cell (1993) 4:1003-1015
#title Fission yeast genes nda4(+) and nda4(+), mutations of which lead to S-phase block, chromatin alteration and Ca(2+) suppression, are members of the CDC46/MCM2 family.
#accession A48723
#status preliminary; not compared with conceptual translation

```

```

##molecule_type DNA
##residues 1-720 ##label MIY
GENETICS
#gene nda4+
KEYWORDS cell division control
FEATURE 319-532 #domain MCM2 core domain similarity #label MCM
SUMMARY #length 720 #molecular-weight 80184 #checksum 1029

Query Match 92.5%; Score 49; DB 11; Length 720;
Best Local Similarity 83.3%; Pred. No. 1.30e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 675 yrmlir 680
|||||
QY 1 YRLLIR 6

RESULT 4
ENTRY S27599 #type complete
TITLE hypothetical protein 3 - Nostoc sp.
ORGANISM #formal_name Nostoc sp.
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
ACCESSIONS S27599
REFERENCE S27596
#authors Walton, D.K.; Gendel, S.M.; Atherly, A.G.
#submission submitted to the EMBL Data Library, February 1992
#accession S27599
#status preliminary
##molecule_type DNA
##residues 1-173 ##label WAL
##cross-references EMBL:M81381
SUMMARY #length 173 #molecular-weight 19346 #checksum 1671

Query Match 90.6%; Score 48; DB 9; Length 173;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 164 yrllir 169
|||||
QY 1 YRLLIR 6

RESULT 5
ENTRY S56263 #type complete
TITLE hypothetical protein YFR008w - yeast (Saccharomyces cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
ACCESSIONS S56263
REFERENCE S56186
#authors Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.; Soeda, E.; Yokoyama, K.; Yamazaki, M.; Tashiro, H.; Eki, T.
#submission submitted to the EMBL Data Library, May 1995
#description Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.
#accession S56263
#status preliminary
##molecule_type DNA
##residues 1-221 ##label MUR
##cross-references EMBL:D50617
GENETICS
#map_position 6R
SUMMARY #length 221 #molecular-weight 25915 #checksum 5555

Query Match 90.6%; Score 48; DB 11; Length 221;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 211 yrllir 216

```

```

QY 1 YRLLIR 6
||||:|
#authors Ogasawara, N.; Yoshikawa, H.
#journal Mol. Microbiol. (1992) 6:629-634
#title Genes and their organization in the replication origin region
of the bacterial chromosome.
#cross-references MUID:92204018
#accession I40440
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type DNA
#residues 1-628 #label RES
#cross-references EXBL:X62539; NID:g40020; CDS_PID:g40026
#experimental_source strain CRK2000
CLASSIFICATION #superfamily gida protein
SUMMARY #length 628 #molecular-weight 69752 #checksum 5500

Query Match 90.6%; Score 48; DB 4; Length 628;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 435 YRLLIR 440
||||:|
QY 1 YRLLIR 6

RESULT 9
ENTRY #type complete
TITLE glucose inhibited division protein (gida) homolog -
ORGANISM Haemophilus influenzae (strain Rd KW20)
#formal_name Haemophilus influenzae
DATE 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
I64078
ACCESSIONS I64078
REFERENCE A64000
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kervage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal Science (1995) 269:496-512
#title Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.
#accession I64078
#status preliminary
#molecule_type DNA
#residues 1-629 #label TIGR
#cross-references GB:L42023; TIGR:HI0582
#note named as homolog to a protein from Escherichia coli
CLASSIFICATION #superfamily gida protein
SUMMARY #length 629 #molecular-weight 70103 #checksum 317

Query Match 90.6%; Score 48; DB 8; Length 629;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 435 YRLLIR 440
||||:|
QY 1 YRLLIR 6

RESULT 10
ENTRY #type complete
TITLE NMD2 protein - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES IFs1 protein; protein YHR077c
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 28-Oct-1994 #sequence_revision 10-Feb-1995 #text_change
06-Sep-1996
ACCESSIONS S48244; S46815; S64648; S64738
REFERENCE S48244
#authors He, F.; Jacobson, A.

```

```

QY 1 YRLLIR 6
||||:|
#authors Ogasawara, N.; Yoshikawa, H.
#journal Mol. Microbiol. (1992) 6:629-634
#title Genes and their organization in the replication origin region
of the bacterial chromosome.
#cross-references MUID:92204018
#accession I40440
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type DNA
#residues 1-628 #label RES
#cross-references EXBL:X62539; NID:g40020; CDS_PID:g40026
#experimental_source strain CRK2000
CLASSIFICATION #superfamily gida protein
SUMMARY #length 628 #molecular-weight 69752 #checksum 5500

Query Match 90.6%; Score 48; DB 11; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 205 YRLLIR 210
||||:|
QY 1 YRLLIR 6

RESULT 7
ENTRY #type complete
TITLE macrolide 3-O-acyltransferase (EC 2.3.1.-) - Streptomyces sp.
ORGANISM #formal_name Streptomyces sp.
DATE 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
14-Jul-1995
ACCESSIONS JC4001
REFERENCE JC4001
#authors Arisawa, A.; Tsunekawa, H.; Okamura, K.; Okamoto, R.
#journal Biosci. Biotechnol. Biochem. (1995) 59:582-588
#title Nucleotide sequence analysis of the carbomycin biosynthetic
genes including the 3-O-acyltransferase gene from
Streptomyces thermotolerans.
#accession JC4001
#molecule_type DNA
#residues 1-389 #label ABI
#cross-references DBJ:D30759
#note the source was designated as Streptomyces thermotolerans
GENETICS acyA
#gene acyltransferase
KEYWORDS #length 389 #molecular-weight 42879 #checksum 3458
SUMMARY

Query Match 90.6%; Score 48; DB 10; Length 389;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 158 YRLLIR 163
||||:|
QY 1 YRLLIR 6

RESULT 8
ENTRY #type complete
TITLE gida protein - Bacillus subtilis
ALTERNATE_NAMES BWBSGA
ORGANISM #formal_name Bacillus subtilis
DATE 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
23-Aug-1996
ACCESSIONS I40440; JQ1216; S18076
REFERENCE I40435

```

```

#submission submitted to the EMBL Data Library, September 1994
#description Identification of a novel component of the nonsense-mediated
#RNA decay pathway using an interacting protein screen.
#accession S48244
##molecule_type DNA
##residues 1-1089 ##label HEF
##cross-references EMBL:U14974
REFERENCE
#authors Favellio, T.
#submission submitted to the EMBL Data Library, June 1994
#description The sequence of S. cerevisiae cosmid 9205.
#accession S46815
##molecule_type DNA
##residues 'MYOQ', 3-1089 ##label FAV
##cross-references EMBL:U10556
REFERENCE
#authors Lee, S.I.; Umen, J.G.; Varmus, H.E.
#journal Proc. Natl. Acad. Sci. U.S.A. (1995) 92:6587-6591
#title A genetic screen identifies cellular factors involved in
retroviral -1 frameshifting.
#accession S64648
##status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-1089 ##label LEE
##cross-references EMBL:U28158
REFERENCE
#authors Varmus, H.E.
#submission submitted to the EMBL Data Library, May 1995
#accession S64738
##molecule_type DNA
##residues 'MYOQ', 3-1089 ##label VAR
##cross-references EMBL:U28158
GENETICS
#gene NMD2; IFS1
#map_position 8R
#introns 2/3
SUMMARY
#length 1089 #molecular-weight 126746 #checksum 7254
Query Match 88.7%; Score 47; DB 11; Length 1089;
Best Local Similarity 83.3%; Pred. No. 2.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 580 Yrllir 585
QY 1 YRLLIR 6
RESULT 11
ENTRY
TITLE
S36116 #type complete
multicatalytic endopeptidase complex (EC 3.4.99.46) chain
PROS-Dm25 - fruitfly (Drosophila melanogaster)
ALTERNATE_NAMES
#proteasome chain PROS-Dm25
ORGANISM
#formal_name Drosophila melanogaster
#formal_revision 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
19-May-1995
DATE
S36116; S36117; A49550
ACCESSIONS
REFERENCE
#authors Seelig, A.; Troxell, M.; Klotzel, P.M.
#journal Blochim. Biophys. Acta (1993) 1174:215-217
#title Sequence and genomic organization of the Drosophila
proteasome PROS-Dm25 gene.
#accession S36116
##molecule_type DNA
##residues 1-234 ##label SE1
##cross-references EMBL:X70304
#accession S36117
##molecule_type protein
#residues 7-36;178-192;228-234 ##label SE2
#note the authors translated the codon ACG for residue 116 as
Pro
REFERENCE
#authors Seelig, A.; Multhaup, G.; Pesold-Hurt, B.; Beyreuther, K.;
Klotzel, P.M.

```

```

#journal J. Biol. Chem. (1993) 268:25561-25567
#title Drosophila proteasome Dm25 subunit substitutes the mouse MC3
subunit in hybrid proteasomes. The N-terminal domain is
essential for subunit incorporation.
#accession A49550
##status not compared with conceptual translation
##molecule_type mRNA
##residues 1-234 ##label SE3
##cross-references GB:X70696
GENETICS
#introns 13/3; 39/3; 125/3; 177/3
#superfamily multicatalytic endopeptidase complex chain C9
#classification hydrolase; proteinase
#keywords
#summary #length 234 #molecular-weight 25906 #checksum 7606
Query Match 86.8%; Score 46; DB 5; Length 234;
Best Local Similarity 66.7%; Pred. No. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 83 Yrllvk 88
QY 1 YRLLIR 6
RESULT 12
ENTRY
TITLE
S38147 #type complete
hypothetical protein YKR070w - yeast (Saccharomyces
cerevisiae)
#formal_name Saccharomyces cerevisiae
#formal_revision 03-May-1994 #sequence_revision 03-May-1994 #text_change
12-Apr-1996
DATE
S38147
ACCESSIONS
REFERENCE
#authors Pohl, T.M.; Pohl, F.M.
#submission submitted to the Protein Sequence Database, March 1994
#accession S38147
##molecule_type DNA
##residues 1-352 ##label POH
#cross-references EMBL:Z28295
#experimental_source strain S288C
GENETICS
#map_position 11R
SUMMARY
#length 352 #molecular-weight 39406 #checksum 754
Query Match 86.8%; Score 46; DB 11; Length 352;
Best Local Similarity 66.7%; Pred. No. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 223 Yrllvr 228
QY 1 YRLLIR 6
RESULT 13
ENTRY
TITLE
C29959 #type complete
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach
chloroplast
#formal_name chloroplast Spinacia oleracea #common_name
spinach
DATE
15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
12-Apr-1995
ACCESSIONS
REFERENCE
#authors Hudson, G.S.; Holton, T.A.; Whitfield, P.R.; Bottomley, W.
#journal J. Mol. Biol. (1988) 200:639-654
#title Spinach chloroplast rpoBC genes encode three subunits of the
chloroplast RNA polymerase.
#cross-references MUID:88316931
#accession C29959
##molecule_type DNA
##residues 1-1070 ##label HUD
##cross-references GB:M55297
GENETICS

```

```
#gene
#genome
CLASSIFICATION #superfamily DNA-directed RNA polymerase beta chain
KEYWORDS chloroplast; nucleotidyltransferase
SUMMARY #length 1070 #molecular-weight 120899 #checksum 2671

Query Match 86.8%; Score 46; DB 5; Length 1070;
Best Local Similarity 66.7%; Pred. No. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1039 frllvr 1044
:||||
Qy 1 YRLLIR 6

RESULT 14
ENTRY #type complete
TITLE DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - common
ORGANISM tobacco chloroplast
#formal_name chloroplast Nicotiana tabacum #common_name
common tobacco
DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
03-Feb-1994
ACCESSIONS A24865; A00690
REFERENCE A24865
#authors Ohme, M.; Tanaka, M.; Chunwongse, J.; Shinozaki, K.; Sugliura,
M.
#journal FEBS Lett. (1986) 200:87-90
#title A tobacco chloroplast DNA sequence possibly coding for a
polypeptide similar to E. coli RNA polymerase beta-subunit.
#cross-references MUID:86192857
#accession A24865
#molecule_type DNA
#residues 1-1070 #label OHM
#cross-references GB:M28017

REFERENCE A38013
#authors Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida,
N.; Matsubayashi, T.; Zaita, N.; Chunwongse, J.; Obokata,
J.; Yamaguchi-Shinozaki, K.; Ohto, C.; Torazawa, K.; Meng,
B.Y.; Sugita, M.; Deno, H.; Kamogashira, T.; Yamada, K.;
Kusuda, J.; Takaiwa, F.; Kato, A.; Tondoh, N.; Shimada, H.;
Sugliura, M.
#journal EMBO J. (1986) 5:2043-2049
#title The complete nucleotide sequence of the tobacco chloroplast
genome: its gene organization and expression.
#contents annotation; gene organization, sites, features
GENETICS
#gene rpoB
#genome chloroplast
CLASSIFICATION #superfamily DNA-directed RNA polymerase beta chain
KEYWORDS chloroplast; nucleotidyltransferase; transcription
SUMMARY #length 1070 #molecular-weight 120546 #checksum 1605

Query Match 86.8%; Score 46; DB 1; Length 1070;
Best Local Similarity 66.7%; Pred. No. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1039 frllvr 1044
:||||
Qy 1 YRLLIR 6

RESULT 15
ENTRY #type complete
TITLE DNA-directed RNA polymerase (EC 2.7.7.6) beta chain : white
mustard chloroplast
ORGANISM #formal_name chloroplast Sinapis alba #common_name white
mustard
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
03-May-1996
ACCESSIONS S48842
REFERENCE S48842
#authors Julicher, K.; Pfannschmidt, T.; Liere, K.; Link, G.
```

```
#submission submitted to the EMBL Data Library, October 1994
#accession S48842
#molecule_type DNA
#residues 1-1078 #label JUL
#cross-references EMBL:X82417

GENETICS
#gene rpoB
#genome chloroplast
CLASSIFICATION #superfamily DNA-directed RNA polymerase beta chain
KEYWORDS chloroplast; nucleotidyltransferase; transcription
SUMMARY #length 1078 #molecular-weight 121669 #checksum 2477

Query Match 86.8%; Score 46; DB 5; Length 1078;
Best Local Similarity 66.7%; Pred. No. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1047 frllvr 1052
:||||
Qy 1 YRLLIR 6

Search completed: Thu May 22 08:30:18 1997
Job time : 20 secs.
```

THIS PAGE BLANK (USPTO)

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA SIMS M.;
 RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
 DR EMBL; Z49967; G886450; -;
 DR WORMPEP; F54C9.5; CE02255.
 KW RIBOSOMAL PROTEIN; RNA-BINDING.
 SQ SEQUENCE 293 AA; 33386 MW; 8FFEC7EE CRC32;

Query Match 85.7%; Score 42; DB 8; Length 293;
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 49 yrlivlr 54
 ||||:|
 QY 1 YRLAIR 6

RESULT 15
 ID YHR4_PSSY STANDARD; PRT; 375 AA.
 AC P20400;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 40 KD PROTEIN IN HRP LOCUS (ORF1).
 OS PSEUDOMONAS SYRINGAE (PV. SYRINGAE).
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
 OC PSEUDOMONADACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R32;
 RX MEDLINE; 89053865.
 RA MUKHOPADHYAY P.; WILLIAMS J.; MILLS D.;
 RL J. BACTERIOL. 170:5479-5488(1988).
 CC -!- FUNCTION: MAY BE INVOLVED IN REGULATION OF HRP OR OTHER HRP LOCI.
 CC -!- SIMILARITY: TO THE C-TERMINAL HALF OF E.COLI MDOG.
 DR EMBL; M23555; -; NOT_ANNOTATED_CDS.
 DR PIR; A31383; A31383.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 375 AA; 41515 MW; 5FB9D42C CRC32;

Query Match 85.7%; Score 42; DB 11; Length 375;
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 219 yrltlr 224
 |||::|
 QY 1 YRLAIR 6

Search completed: Thu May 22 08:31:19 1997
 Job time : 11 secs.

Query Match 85.7%; Score 42; DB 1; Length 148;
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 132 yklav1 137
 |::|:
 QY 1 YRLAIR 6

RESULT 11
 ID COAT_CTV36 STANDARD; PRT; 223 AA.
 AC Q00686;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE COAT PROTEIN.
 OS CITRUS TRISTEZA VIRUS (ISOLATE T36) (CTV).
 OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CAPILLOVIRIDAE.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-38.
 RX MEDLINE: 91237334.
 RA SEKIYA M.E., LAWRENCE S.D., MCCAFFERY M., CLINE K.;
 RL J. GEN. VIROL. 72:1013-1020(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94160579.
 RA PAPPU H.R., KARASEV A.V., ANDERSON E.J., PAPPU S.S., HILF M.E.,
 RA FEBRES V., ECKLOFF R.M.G., MCCAFFERY M., BOYKO V., GOWDA S.,
 RA DOLJA V.V., KOONIN E.V.;
 RL VIROLOGY 199:35-46(1994).
 CC -!- PTM: CONSISTS OF AT LEAST TWO SIZE VARIANTS, CP1 AND CP2, WHICH
 CC RESULT OF POST-TRANSLATIONAL PROTEOLYSIS AT SITES APPROXIMATIVELY
 CC 12 TO 15 AND 26 AA FROM THE N-TERMINUS RESPECTIVELY.
 DR EMBL: M76485; G323416; -.
 DR EMBL: U16304; G806746; -.
 KW COAT PROTEIN.
 SQ SEQUENCE 223 AA; 24909 MW; F3AA6BB6 CRC32;

Query Match 85.7%; Score 42; DB 2; Length 223;
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 85 yrlavk 90
 |::|:
 QY 1 YRLAIR 6

RESULT 12
 ID FRDC_WOLSU STANDARD; PRT; 256 AA.
 AC P17413;
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE FUMARATE REDUCTASE CYTOCHROME B SUBUNIT.
 GN FRDC.
 OS WOLINELLA SUCCINOGENES.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC RODS;
 OC BACTEROIDACEAE.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE: 90355847.
 RA KOERTNER C., LAUTERBACH F., TRIPIER D., UNDEN G., KROEGER A.;
 RL MOL. MICROBIOL. 4:855-860(1990).
 CC -!- FUNCTION: DI-HEME CYTOCHROME OF THE FUMARATE REDUCTASE COMPLEX.
 CC -!- SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING THREE SUBUNITS;
 CC A FLAVOPROTEIN, AN IRON-SULFUR PROTEIN AND A CYTOCHROME B.
 CC -!- SIMILARITY: TO CYTOCHROME B-558 FROM B.SUBTILIS SUCCINATE
 CC DEHYDROGENASE.
 DR EMBL: X51509; G48512; -.
 DR FIR: S10184; S10164.
 KW TRICARBOXYLIC ACID CYCLE; TRANSMEMBRANE; ELECTRON TRANSPORT; HEME.
 FT TRANSMEM 32 54
 FT TRANSMEM 77 98
 FT POTENTIAL.

FT TRANSMEM 123 149 POTENTIAL.
 FT TRANSMEM 171 192 POTENTIAL.
 FT TRANSMEM 214 232 POTENTIAL.
 FT BINDING 44 44 HEME (POTENTIAL).
 FT BINDING 93 93 HEME (POTENTIAL).
 FT BINDING 143 143 HEME (POTENTIAL).
 FT BINDING 182 182 HEME (POTENTIAL).
 SQ SEQUENCE 256 AA; 29723 MW; C3AB8928 CRC32;

Query Match 85.7%; Score 42; DB 4; Length 256;
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 188 yrlavk 193
 |::|:
 QY 1 YRLAIR 6

RESULT 13
 ID YIAJ_HAEIN STANDARD; PRT; 268 AA.
 AC P44996;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1032.
 GN HI1032.
 OS HAEMOPHILUS INFLUENZAE.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC PASTEURILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-RD / KW20;
 RX MEDLINE: 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RL SCIENCE 269:496-512(1995).
 CC -!- SIMILARITY: STRONG, TO E.COLI YIAJ.
 CC -!- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: L45670; G1006264; -.
 DR EMBL: U32784; G926093; -.
 DR PROSITE: PS01051; HTH_ICLR_FAMILY.
 KW HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING.
 FT DNA_BIND 37 56 H-T-H MOTIF (POTENTIAL).
 SQ SEQUENCE 268 AA; 30580 MW; B5AA0AEB CRC32;

Query Match 85.7%; Score 42; DB 11; Length 268;
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 73 yrltik 78
 |::|:
 QY 1 YRLAIR 6

RESULT 14
 ID RL5_CAEEL STANDARD; PRT; 293 AA.
 AC P49405;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE PROBABLE 60S RIBOSOMAL PROTEIN L5.
 GN F54C9.5.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 RN [1]

RX MEDLINE; 94014976.
 RA ARHIN F.F., VINING L.C.;
 RL J. GEN. MICROBIOL. 139:1785-1793(1993).
 CC -!- FUNCTION: CATALYZES THE BIOSYNTHESIS OF 4-AMINO-4-DEOXYCHORISMATE
 CC -!- (ADC) FROM CHORISMATE AND GLUTAMINE.
 CC -!- PATHWAY: FOLATE BIOSYNTHESIS PATHWAY. FIRST STEP IN THE
 CC BIOSYNTHESIS OF P-AMINOBENZOATE (PABA).
 CC -!- SUBUNIT: CONSISTS OF TWO NONIDENTICAL CHAINS: COMPONENT I
 CC CATALYZES THE FORMATION OF ADC BY BINDING CHORISMATE AND AMMONIA;
 CC COMPONENT II PROVIDES THE GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
 DR EMBL; M64860; G149462; -
 KW LYASE; FOLATE BIOSYNTHESIS.
 SQ SEQUENCE 470 AA; 50970 MW; 41AC304B CRC32;

Query Match 87.8%; Score 43; DB 7; Length 470;

Best Local Similarity 83.3%; Pred. No. 1.28e+01;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 411 yrlair 416
 |||||
 QY 1 YRLAIR 6

RESULT 8

ID ARO1_EME1 STANDARD; PRT; 1603 AA.
 AC P07547;
 DT 01-APR-1988 (REL. 07, CREATED)
 DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE PENTAFUNCTIONAL AROM POLYPEPTIDE (CONTAINS: 3-DEHYDROQUINATE SYNTHASE
 DE (EC 4.6.1.3), 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10)
 DE (3-DEHYDROQUINASE), SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25), SHIKIMATE
 DE KINASE (EC 2.7.1.71), AND EPSP SYNTHASE (EC 2.5.1.19)).
 GN AROMA OR AROM.
 OS EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
 CC EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R153;
 RX MEDLINE; 86176723.
 RA CHARLES I.G., KEYTE J.W., BRAMMAR W.J., SMITH M., HAWKINS A.R.;
 RL NUCLEIC ACIDS RES. 14:2201-2213(1986).
 RN [2]
 RP SEQUENCE OF 844-1474 FROM N.A.
 RX MEDLINE; 86067221.
 RA CHARLES I.G., KEYTE J.W., BRAMMAR W.J., HAWKINS A.R.;
 RL NUCLEIC ACIDS RES. 13:8119-8128(1985).
 CC -!- FUNCTION: THE AROM POLYPEPTIDE CATALYZES 5 CONSECUTIVE ENZYMAIC
 CC REACTIONS IN PRECHORISMATE POLYAROMATIC AMINO ACID BIOSYNTHESIS.
 CC -!- PATHWAY: SECOND TO SIXTH STEP IN THE BIOSYNTHESIS FROM CHORISMATE
 CC OF THE AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -!- CATALYTIC ACTIVITY: 7-PHOSHO-3-DEOXY-ARABINO-HEPTULOSONATE -
 CC 3-DEHYDROQUINATE + ORTHOPHOSPHATE.
 CC -!- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE = 3-DEHYDROSHIKIMATE + H(2)O.
 CC -!- CATALYTIC ACTIVITY: SHIKIMATE + NADP(+) = 5-DEHYDROSHIKIMATE +
 CC NADPH.
 CC -!- CATALYTIC ACTIVITY: ADP + SHIKIMATE = ADP + SHIKIMATE 3-PHOSPHATE.
 CC -!- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHIKIMATE =
 CC ORTHOPHOSPHATE + O(5)-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE.
 DR EMBL; X05204; G2333; -
 DR PIR; A24962; BVASAL1.
 DR PIR; A24042; A24042.
 DR PROSITE; PS00104; EPSP SYNTHASE_1.
 DR PROSITE; PS00885; EPSP SYNTHASE_2.
 DR PROSITE; PS01028; DEHYDROQUINASE_1.
 DR PROSITE; PS01128; SHIKIMATE_KINASE.
 KW AROMATIC AMINO ACID BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME;
 KW OXIDOREDUCTASE; LYASE; TRANSFERASE; KINASE; NADP; ATP-BINDING.
 FT DOMAIN 1 384
 FT DOMAIN 397 843
 FT DOMAIN 863 1056
 FT DOMAIN 1057 1277
 FT DOMAIN 1290 1603
 SHIKIMATE DEHYDROGENASE.

FT ACT_SITE 825 825 POTENTIAL.
 FT NP_BIND 871 878 ATP (BY SIMILARITY).
 FT ACT_SITE 1180 1180 BY SIMILARITY.
 FT ACT_SITE 1208 1208 FORMS A SCHIFF-BASE INTERMEDIATE
 SQ SEQUENCE 1603 AA; 175094 MW; 26E56D97 CRC32;
 (BY SIMILARITY).

Query Match 87.8%; Score 43; DB 1; Length 1603;
 Best Local Similarity 83.3%; Pred. No. 1.28e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1141 yrlair 1146
 |||||
 QY 1 YRLAIR 6

RESULT 9

ID V187_BPT3 STANDARD; PRT; 83 AA.
 AC P10302;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-MAR-1989 (REL. 10, LAST ANNOTATION UPDATE)
 DE GENE 18.7 PROTEIN.
 GN 18.7.
 OS BACTERIOPHAGE T3.
 CC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PODOVIRIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86209997.
 RA YAMADA M., FUJISAWA H., KATO H., HAMADA K., MINAGAWA T.;
 RL VIROLOGY 151:350-361(1986).
 RN [2]
 RP ERRATUM.
 RA YAMADA M., FUJISAWA H., KATO H., HAMADA K., MINAGAWA T.;
 RL VIROLOGY 154:246-246(1986).
 DR EMBL; M14784; G1196765; -
 DR PIR; E23476; W8BPT3.
 SQ SEQUENCE 83 AA; 9393 MW; 6D9B1F91 CRC32;

Query Match 85.7%; Score 42; DB 10; Length 83;

Best Local Similarity 66.7%; Pred. No. 2.15e+01;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 20 yrlsik 25
 |||||
 QY 1 YRLAIR 6

RESULT 10

ID 3DHQ_BACSU STANDARD; PRT; 148 AA.
 AC P54517;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE PUTATIVE CATABOLIC 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-
 DEHYDROQUINASE).
 GN YQHS.
 OS BACILLUS SUBTILIS.
 CC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / JH642;
 RA KOSAYASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S.,
 RA SATO T., TAKEUCHI M.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE = 3-DEHYDROSHIKIMATE + H(2)O.
 CC -!- PATHWAY: SECOND STEP OF THE QUINIC ACID CATABOLIC PATHWAY.
 CC -!- SIMILARITY: BELONGS TO THE TYPE-II 3-DEHYDROQUINASE FAMILY.
 DR EMBL; D84432; G1303900; -
 DR SUBTILIS; BG11707; YQHS.
 KW HYPOTHETICAL PROTEIN; QUINATE METABOLISM; LYASE.
 SQ SEQUENCE 148 AA; 16431 MW; B2D0F289 CRC32;

```

RESULT 4
ID TCPAARATH STANDARD; PRT; 545 AA.
AC P28769;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DE 60S RIBOSOMAL PROTEIN L1 (L5) (YLL3) (RIBOSOMAL 5 S RNA-BINDING
DE T-COMPLEX PROTEIN L1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA).
GN CCT1.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA: PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALE; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93138412.
RA MORI M., MURATA K., KUBOTA H., YAMAMOTO A., MATSUSHIRO A.,
RA MORITA T.;
RA GENE 122:381-382(1992).
CC -1- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
CC ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
CC ACTIN AND TUBULIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 KD THAT
CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.
CC -1- SIMILARITY: TO OTHER MEMBERS OF TCP-1 CHAPERONIN FAMILY.
DR EMBL: D11351; G217871; -
DR PIR: JN0448; JN0448.
DR PROSITE; PS00750; TCPI_1.
DR PROSITE; PS00751; TCPI_2.
DR PROSITE; PS00995; TCPI_3.
KW CHAPERONE; ATP-BINDING; MULTIGENE FAMILY.
SQ SEQUENCE 545 AA; 59229 MW; 8E52A94B CRC32;

Query Match 89.8%; Score 44; DB 9; Length 545;
Best Local Similarity 83.3%; Pred. No. 7.58e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 124 yrlamr 129
QY 1 YRLAIR 6

RESULT 5
ID RL5_SCHPO STANDARD; PRT; 293 AA.
AC P52822;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE 60S RIBOSOMAL PROTEIN L5.
GN RPL5.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96212235.
RA MICHAEL W.M., DREYFUSS G.;
RA J. BIOL. CHEM. 271:11571-11574(1996).
CC -1- FUNCTION: THIS PROTEIN BINDS 5S RNA.
CC -1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
DR EMBL: U48270; G1206017; -
KW RIBOSOMAL PROTEIN.
SQ SEQUENCE 293 AA; 33255 MW; 4D72400A CRC32;

Query Match 87.8%; Score 43; DB 8; Length 293;
Best Local Similarity 66.7%; Pred. No. 1.28e+01;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 48 yrlvvr 53
QY 1 YRLAIR 6

RESULT 6

```

```

ID RLL_YEAST STANDARD; PRT; 297 AA.
AC P26321;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DE 60S RIBOSOMAL PROTEIN L1 (L5) (YL3) (RIBOSOMAL 5 S RNA-BINDING
DE PROTEIN).
GN RPL1 OR YPL131W OR LPL14W.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX MEDLINE; 91177855.
RA TANG B., NAZAR R.N.;
RA J. BIOL. CHEM. 266:6120-6123(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92388126.
RA TANG B., NAZAR R.N.;
RA J. BIOL. CHEM. 267:17738-17742(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90360986.
RA TZAGOLOFF A., CAPITANTO N., NOBREGA M.P., GATTI D.;
RA EMBO J. 9:2759-2764(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93233645.
RA DESHMUKH M.P., TSAY Y.F., PAULOVICH A.G., WOOLFORD J.L.;
RA MOL. CELL. BIOL. 13:2835-2845(1993).
RN [5]
RP SEQUENCE FROM N.A.
RA HALL J., DEPAULO T., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D.,
RA STORMS R.K., VO D.H., WANG Y., WINNETT E.;
RA SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: THIS PROTEIN BINDS 5S RNA.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
DR EMBL: M65036; G173232; -
DR EMBL: M94864; G173235; -
DR EMBL: L01796; G172424; -
DR EMBL: U43703; G1244783; -
DR PIR: S14172; S14172.
DR PIR: S48089; S48089.
DR LISTA; SC01009; RPL1.
DR SGD; L0001699; RPL1.
KW RIBOSOMAL PROTEIN; RNA-BINDING.
FT CONFLICT 112 112 R -> K (IN REF. 4 AND 5).
SQ SEQUENCE 297 AA; 33743 MW; 2D9F1304 CRC32;

Query Match 87.8%; Score 43; DB 8; Length 297;
Best Local Similarity 66.7%; Pred. No. 1.28e+01;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 49 yrlvvr 54
QY 1 YRLAIR 6

RESULT 7
ID PABP_LACLA STANDARD; PRT; 470 AA.
AC P27629;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DE 60S RIBOSOMAL PROTEIN L1 (L5) (YL3) (RIBOSOMAL 5 S RNA-BINDING
DE PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-) (ADC SYNTHASE).
GN PABP.
OS LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).
OC PROKARYOTA; FIRMICUTES; COCCI; STREPTOCOCCAEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCD0 496;

```

WISREH
***** (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:31:08 1997; MasPar time 1.96 Seconds
Tabular output not generated. 64.775 Million cell updates/sec

Title: >US-08-653-294-7
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 YRLAIR 6

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 22.440; Variance 22.471; scale 0.999

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|-----------------------------------|
| 1 | 46 | 93.9 | 1333 | 8 | RPOA_SCHPO | RETROTRANSPPOSABLE ELE 2.57e+00 |
| 2 | 45 | 91.8 | 1132 | 10 | VHSJ_LAMBD | HOST SPECIFICITY PROT 4.44e+00 |
| 3 | 45 | 91.8 | 2616 | 6 | NDL_DROME | SERINE PROTEASE NUDEL 4.44e+00 |
| 4 | 44 | 89.8 | 545 | 9 | TCPLA_ARATH | T-COMPLEX PROTEIN 1, 7.58e+00 |
| 5 | 43 | 87.8 | 293 | 8 | RL5_SCHPO | 60S RIBOSOMAL PROTEIN 1, 1.28e+01 |
| 6 | 43 | 87.8 | 297 | 8 | RL1_YEAST | 60S RIBOSOMAL PROTEIN 1, 1.28e+01 |
| 7 | 43 | 87.8 | 470 | 7 | PABB_LACLA | PARA-AMINOBENZONATE SY 1.28e+01 |
| 8 | 43 | 87.8 | 1603 | 1 | ARO1_EMENI | PENTAFUNCTIONAL AROM 1.28e+01 |
| 9 | 42 | 85.7 | 83 | 10 | V187_BPT3 | GENE 18.7 PROTEIN. 2.15e+01 |
| 10 | 42 | 85.7 | 148 | 1 | 3DHQ_BACSU | PUTATIVE CATABOLIC 3- 2.15e+01 |
| 11 | 42 | 85.7 | 223 | 2 | COAT_CTV36 | COAT PROTEIN. 2.15e+01 |
| 12 | 42 | 85.7 | 256 | 4 | FRC_CWLSU | FUMARATE REDUCTASE CY 2.15e+01 |
| 13 | 42 | 85.7 | 268 | 11 | YIAJ_HAEIN | HYPOTHETICAL TRANSERI 2.15e+01 |
| 14 | 42 | 85.7 | 293 | 8 | RL5_CAPEL | PROBABLE 60S RIBOSOMA 2.15e+01 |
| 15 | 42 | 85.7 | 375 | 11 | YHR4_PSESY | HYPOTHETICAL 40 KD PR 2.15e+01 |
| 16 | 42 | 85.7 | 397 | 3 | DP3B_MYCSM | DNA POLYMERASE III, B 2.15e+01 |
| 17 | 42 | 85.7 | 399 | 3 | DP3B_MYCLE | DNA POLYMERASE III, B 2.15e+01 |
| 18 | 42 | 85.7 | 621 | 3 | DCTE_RHIME | C4-DICARBOXYLATE TRAN 2.15e+01 |
| 19 | 42 | 85.7 | 937 | 1 | ADAC_RAT | ALPHA-ADAPTIN (C) (CL 2.15e+01 |
| 20 | 42 | 85.7 | 938 | 1 | ADAC_MOUSE | ALPHA-ADAPTIN (C) (CL 2.15e+01 |
| 21 | 42 | 85.7 | 958 | 5 | HIG_DROME | LOCOMOTION-RELATED PR 2.15e+01 |
| 22 | 42 | 85.7 | 977 | 1 | ADRA_MOUSE | ALPHA-ADAPTIN (A) (CL 2.15e+01 |

| | | | | | | |
|----|----|------|------|---|------------|---------------------------------|
| 23 | 42 | 85.7 | 1538 | 9 | SIN3_YEAST | PAIRED AMPHIPATHIC HE 2.15e+01 |
| 24 | 42 | 85.7 | 1692 | 3 | CYAA_SCHPO | ADENYLATE CYCLASE (EC 2.15e+01 |
| 25 | 42 | 85.7 | 2035 | 5 | HMP2_YEREN | HIGH-MOLECULAR-WEIGHT 3.56e+01 |
| 26 | 41 | 83.7 | 349 | 6 | NTRB_SALTY | NITROGEN REGULATION P 3.56e+01 |
| 27 | 41 | 83.7 | 349 | 6 | NTRB_ECOLI | NITROGEN REGULATION P 3.56e+01 |
| 28 | 41 | 83.7 | 353 | 8 | PSBA_MARPO | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 29 | 41 | 83.7 | 360 | 8 | PSBA_SYNY4 | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 30 | 41 | 83.7 | 360 | 8 | PSBA_ANTSP | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 31 | 41 | 83.7 | 360 | 8 | PSBA_PREDI | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 32 | 41 | 83.7 | 360 | 8 | PSBA_PROMA | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 33 | 41 | 83.7 | 360 | 8 | PSB2_SYNEH | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 34 | 41 | 83.7 | 360 | 8 | PSB1_SYNY3 | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 35 | 41 | 83.7 | 360 | 8 | PSB1_SYNYU | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 36 | 41 | 83.7 | 360 | 8 | PSB1_SYNP7 | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 37 | 41 | 83.7 | 360 | 8 | PSB1_ANASP | PHOTOSYSTEM Q(B) PROT 3.56e+01 |
| 38 | 41 | 83.7 | 410 | 6 | MDP1_RABIT | MICROSOMAL DIBEPIDAS 3.56e+01 |
| 39 | 41 | 83.7 | 446 | 1 | AP50_SCHPO | PUTATIVE CLATHRIN COA 3.56e+01 |
| 40 | 41 | 83.7 | 620 | 4 | HENA_MEASY | HEMAGGLUTININ-NEURAMI 3.56e+01 |
| 41 | 41 | 83.7 | 626 | 3 | DPO2_SULSO | DNA POLYMERASE II (EC 3.56e+01 |
| 42 | 41 | 83.7 | 732 | 1 | ACPH_HUMAN | ACYLAMINO-ACID-RELEASE 3.56e+01 |
| 43 | 41 | 83.7 | 732 | 1 | ACPH_RAT | ACYLAMINO-ACID-RELEASE 3.56e+01 |
| 44 | 41 | 83.7 | 782 | 3 | DPO2_ECOLI | DNA POLYMERASE II (EC 3.56e+01 |
| 45 | 41 | 83.7 | 1997 | 8 | PTPB_HUMAN | PROTEIN-TYROSINE PHOS 3.56e+01 |

ALIGNMENTS

RESULT 1
ID RPOA_SCHPO STANDARD; PRT; 1333 AA.
AC Q05654;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE RETROTRANSPPOSABLE ELEMENT TF2 155 KD PROTEIN.
GN SPAC26A3.13C.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE; 93380663.
RA WEAVER D.C., SHPAKOVSKI G.V., CAPUTO E., LEVIN H.L., BOEKE J.D.;
RL GENE 131:135-139(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA MCLEAN J., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SIMILARITY: REGIONALLY, TO PROTEASE, REVERSE TRANSCRIPTASE,
CC RNASE H AND INTEGRASE FROM OTHER RETROTRANSPPOSONS AND
CC RETROVIRUSES.
DR EMBL; L10324; G173439; -.
DR EMBL; Z69240; E220685; -.
KW TRANSPOSABLE ELEMENT.
FT SIMILAR 1 400 TO CAPSID PROTEIN FROM RETROVIRUSES.
FT CONFLICT 206 206 L->P (IN REF. 1).
SQ SEQUENCE 1333 AA; 154932 MW; 78D5D7DA CRC32;

Query Match 93.9%; Score 46; DB 8; Length 1333;
Best Local Similarity 83.3%; Pred. No. 2.57e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 411 yr1pir 416
|||:
|||:
Qy 1 YRLAIR 6

RESULT 2
ID VHSJ_LAMBD STANDARD; PRT; 1132 AA.
AC P03749;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)

WQSELEH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:30:35 1997; MasPar time 1.92 Seconds

Tabular output not generated. 34.026 Million cell updates/sec

Title: >US-08-653-294-6
Description: (1-6) from US08653294.pep
Perfect Score: 53
Sequence: 1 YRLIIR 6

Scoring table:
PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 16.490; Variance 45.535; scale 0.362

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|------------------------|-----------|
| 1 | 48 | 90.6 | 389 | R15428 | 3-acetylation enzyme. | 4.52e+01 |
| 2 | 47 | 88.7 | 724 | R93081 | Bacillus thuringiensis | 5.89e+01 |
| 3 | 47 | 88.7 | 764 | W01897 | Nonsense-mediated MRN | 5.89e+01 |
| 4 | 47 | 88.7 | 1089 | W01896 | Nonsense-mediated MRN | 5.89e+01 |
| 5 | 46 | 86.8 | 43 | R15902 | Drosophila-12 cadher | 7.66e+01 |
| 6 | 46 | 86.8 | 43 | R87142 | Protocadherin clone D | 7.66e+01 |
| 7 | 45 | 84.9 | 434 | R93698 | Erythrocyte longus | 9.94e+01 |
| 8 | 44 | 83.0 | 4472 | R97246 | Virulence gene cluste | 1.29e+02 |
| 9 | 43 | 81.1 | 10 | R61548 | Peptide fragment (1.0 | 1.66e+02 |
| 10 | 43 | 81.1 | 158 | R12458 | HPV18 E6/E7 proteins. | 1.66e+02 |
| 11 | 43 | 81.1 | 158 | R79656 | HPV-18 E6 protein. | 1.66e+02 |
| 12 | 43 | 81.1 | 271 | R27728 | HPV 18 E6 protein fra | 1.66e+02 |
| 13 | 43 | 81.1 | 451 | R27642 | Human calcium channel | 1.66e+02 |
| 14 | 43 | 81.1 | 652 | R63808 | Human amphotropic ret | 1.66e+02 |
| 15 | 43 | 81.1 | 1592 | R32925 | Glucosyltransferase | 1.66e+02 |
| 16 | 43 | 81.1 | 4987 | R10834 | Rianodin receptor. | 1.66e+02 |
| 17 | 43 | 81.1 | 5035 | R25450 | MH mutant porcine rya | 1.66e+02 |
| 18 | 43 | 81.1 | 5072 | R15110 | Ryanodine receptor de | 1.66e+02 |
| 19 | 42 | 79.2 | 12 | R93429 | HLA-B2702 84-79-84 pa | 2.15e+02 |
| 20 | 42 | 79.2 | 20 | R95428 | HLA-B2702 84-75-84 pa | 2.15e+02 |

21 79.2 20 18 R95430
22 42 79.2 20 16 R92907
23 42 79.2 20 16 R92909
24 42 78.2 20 16 R92911
25 42 79.2 78 7 R92925
26 42 79.2 205 7 R93353
27 42 79.2 402 10 R54204
28 42 79.2 643 18 R97735
29 42 79.2 643 1 R91462
30 42 78.2 772 15 R79949
31 42 79.2 775 15 R79950
32 42 78.2 3079 11 R59926
33 41 77.4 64 15 R78151
34 41 77.4 108 18 R93159
35 41 77.4 391 12 R63233
36 41 77.4 457 14 R78184
37 41 77.4 501 13 R62115
38 41 77.4 501 17 R81471
39 41 77.4 1025 8 R38863
40 41 77.4 1047 3 R10867
41 41 77.4 1047 3 R10399
42 41 77.4 3077 1 R93283
43 41 77.4 3211 1 R81769
44 40 75.5 169 19 W05507
45 40 75.5 1138 8 R39820

HLA-B2702 84-75T/75-8 2.15e+02
HLA-B2702 CTL modulat 2.15e+02
HLA-B2702 CTL modulat 2.15e+02
HLA-B2702 CTL modulat 2.15e+02
Hydrophobic protein d 2.15e+02
EpiQ protein. 2.15e+02
snac gene product inv 2.15e+02
Bacillus thuringiensis 2.15e+02
67-kD protein toxin. 2.15e+02
Enzyme W-11. 2.15e+02
Enzyme Q36. 2.15e+02
GAP protein Ira2. 2.15e+02
zebrafish sonic hedge 2.76e+02
Murine monoclonal ant 2.76e+02
ATP-sensitive K chann 2.76e+02
E.coli cell division 2.76e+02
Nocardia coralina al 2.76e+02
Nocardia coralina al 2.76e+02
GC-B. 2.76e+02
NPRB(Pro655, Glu656, 2.76e+02
Human Natriuretic Pep 2.76e+02
Sequence of clone HIV 2.76e+02
Sequence encoded by t 2.76e+02
HCMV Toledo strain UL 3.54e+02
tie receptor kinase. 3.54e+02

ALIGNMENTS

RESULT 1
ID R15428 standard; Protein; 389 AA.
AC R15428;
DT 25-FEB-1992 (first entry)
DE 3-acetylation enzyme.
KW Macrolide antibiotics; acylation; Streptomyces; tylosin;
KW spiramycin; leucomycin; nidamycin; acya.
OS Streptomyces thermotolerans ATCC 11416.
PN EP-459525-A.
PD 04-DEC-1991.
PF 03-JUN-1991; 109033.
PR 01-JUN-1990; JP-141625.
PR 22-FEB-1991; JP-048753.
PA (SAOC) MERCIAN CORP.
PI Arisawa A, Kawamura N, Kojima I, Tone H, Okamoto R;
PI Okamura K.
DR WPI; 91-355809/49.
DR N-PSDB; Q14978.
PT Gene encoding 3-acetylation enzyme for macrolide antibiotics - used
PT to transform Streptomyces sp. to have acylation activity, for use
in medicine.
PS Disclosure; Fig 7: 45pp; English.
CC The sequence was deduced from DNA sequence obtd. from plasmid p53A,
CC a subclone of a DNA library prepd. from genomic DNA of S.thermotol-
CC erans. The 3-acetylation enzyme is involved in the synthesis of
CC macrolide antibiotics. Microorganisms, ep. Streptomyces, trans-
CC formed with the gene can be used for the commercial prodn. of
CC macrolide antibiotics, e.g. 3-acetylated tylosin.
SQ Sequence 389 AA;
Query Match 90.6%; Score 48; DB 3; Length 389;
Best Local Similarity 83.3%; Pred. No. 4.52e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 158 yrlIIR 163
Qy 1 YRLIIR 6
RESULT 2
ID R93081 standard; Protein; 724 AA.
AC R93081;
DT 04-OCT-1996 (first entry)
DE Bacillus thuringiensis insecticidal protein JEG80.

KW Insecticidal crystal toxin; jeg80; anti-diptera; mosquito; larvae;
 OS Aedes aegypti; Anopheles stephensi; Culex pipiens; Btjcg 367.
 PN Bacillus thuringiensis ser. jegathesan 367.
 WO9606171-A2.
 PD 29-FEB-1996.
 PF 24-AUG-1995; F01116.
 PR 25-AUG-1994; FR-010299.
 PA (INSP) INST PASTEUR.
 PI Delecluse A, Thierry I;
 DR WPI; 96-151374/15.
 DR N-PSDB; T17044.
 PT New B.thuringiensis ser. jegathesan insecticidal proteins - and
 PT related DNA, with high activity against dipteran larvae, e.g.
 PT A.aegypti, A.stephensi or C.pipiens
 PS Claim 17; Fig 5; 55pp; French.
 CC The present sequence is that of the JEG80 protein which was isolated
 CC from Bacillus thuringiensis ser. Jegathesan 367 (Btjcg367); it is
 CC a crystal toxin of mol. wt. 80 kD which is active against dipteran
 CC insects, esp. mosquitoes. The full-length, recombinant JEG80 toxin,
 CC had mean LC50 values (in ng/ml) after 48 hours of 18.8, 42.7 and
 CC 10.1 against larvae of Aedes aegypti, Anopheles stephensi and Culex
 CC pipiens, respectively. Wild-type Btjcg367 crystals gave values of
 CC 47.4, 54.5 and 9.6. The JEG80 protein is far more toxic (6-40 times
 CC more toxic against the mosquito species tested) than the Bt CryIVD
 CC toxin, despite their close sequence similarity.
 SQ Sequence 724 AA;

Query Watch 88.7%; Score 47; DB 18; Length 724;
 Best Local Similarity 83.3%; Pred. No. 5.89e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 548 yrlilr 553
 |||||
 QY 1 YRLILR 6

RESULT 3
 ID W01897 standard; Protein; 764 AA.
 AC W01897;
 DT 24-NOV-1996 (first entry)
 DE Nonsense-mediated mRNA decay 2 C-terminal.
 KW Nonsense-mediated mRNA decay; NMD2; Upflp; inhibition.
 OS Saccharomyces cerevisiae.
 PN WO9622301-A1.
 PD 25-JUL-1996.
 PF 27-DEC-1995; U16930.
 PR 20-JAN-1995; US-375300.
 PA (UYNA-) UNIV MASSACHUSETTS MEDICAL CENT.
 PI He F, Jacobson AS;
 DR WPI; 96-354469/35.
 DR N-PSDB; T31994.
 PT Isolated nonsense-mediated mRNA decay gene and protein - used to
 PT develop methods for inhibiting the decay pathway for producing
 PT heterologous or endogenous proteins
 PS Claim 10; Page 54-56; 73pp; English.
 CC The NMD2 gene (T31993) is named after its role in the Nonsense-
 CC Mediated mRNA Decay pathway. The protein, Nmd2p, binds to Upflp.
 CC A C-terminal fragment of the protein (T31994) also binds Upflp and,
 CC when overexpressed in the host cell, the fragment inhibits the
 CC function of Upflp, thereby inhibiting the nonsense-mediated
 CC mRNA decay pathway.
 SQ Sequence 764 AA;

Query Watch 88.7%; Score 47; DB 19; Length 764;
 Best Local Similarity 83.3%; Pred. No. 5.89e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 255 yrlilr 260
 |||||
 QY 1 YRLILR 6

RESULT 4

ID W01896 standard; Protein; 1089 AA.
 AC W01896;
 DT 24-NOV-1996 (first entry)
 DE Nonsense-mediated mRNA decay 2 protein.
 KW Nonsense-mediated mRNA decay; NMD2; Upflp; inhibition.
 OS Saccharomyces cerevisiae.
 PN WO9622301-A1.
 PD 25-JUL-1996.
 PF 27-DEC-1995; U16930.
 PR 20-JAN-1995; US-375300.
 PA (UYNA-) UNIV MASSACHUSETTS MEDICAL CENT.
 PI He F, Jacobson AS;
 DR WPI; 96-354469/35.
 DR N-PSDB; T31993.
 PT Isolated nonsense-mediated mRNA decay gene and protein - used to
 PT develop methods for inhibiting the decay pathway for producing
 PT heterologous or endogenous proteins
 PS Claim 8; Page 49-52; 73pp; English.
 CC The NMD2 gene (T31993) is named after its role in the Nonsense-
 CC Mediated mRNA Decay pathway. The protein, Nmd2p, binds to Upflp.
 CC A C-terminal fragment of the protein (T31994) also binds Upflp and,
 CC when overexpressed in the host cell, the fragment inhibits the
 CC function of Upflp, thereby inhibiting the nonsense-mediated
 CC mRNA decay pathway.
 SQ Sequence 1089 AA;

Query Watch 88.7%; Score 47; DB 19; Length 1089;
 Best Local Similarity 83.3%; Pred. No. 5.89e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 580 yrlilr 585
 |||||
 QY 1 YRLILR 6

RESULT 5
 ID R58902 standard; Protein; 43 AA.
 AC R58902;
 DT 17-APR-1995 (first entry)
 DE Drosophila-12 cadherin-related molecule.
 KW Cadherin; cell adhesion molecule.
 OS Drosophila.
 PN WO9414960-A.
 PD 07-JUL-1994.
 PF 23-DEC-1993; U12588.
 PR 29-DEC-1992; US-998003.
 PA (DOHE-) DOHENY EYE INST.
 PI Suzuki S;
 DR WPI; 94-293849/36.
 DR N-PSDB; O68993.
 PT Polynucleotide sequences encoding new proto:cadherins - useful
 PT for modulating natural binding and regulating activities.
 PS Example; Page 63; 114pp; English.
 CC Two regions of conserved AA sequence, one from the middle of the
 CC third cadherin extracellular subdomain (EC-3) and the other from the
 CC C-terminus of the fourth extracellular subdomain (EC-4) were
 CC identified. The corresp. degenerate oligos (Q68949, Q68950) were
 CC designed for use as PCR primers. PCR was carried out on a rat brain
 CC cDNA prep. Two major bands of about 450 bps and 130 bps were found.
 CC The 450 bp band corresponded to the expected length between the two
 CC primer sites, but the 130 bp band could not be predicted from any
 CC of the previously identified cadherin sequences. The 450 bp and 130
 CC bp bands were extracted and sequenced. Nineteen novel partial cDNA
 CC clones were isolated. The DNA and deduced AA sequences of the
 CC clones (including sequences corresp. to the PCR primers) are given
 CC in Q68951-Q68969 and R58860-R58878. Various cDNA fragments
 CC structurally similar to the rat cDNAs were isolated from human,
 CC mouse and Xenopus brain cDNA preps. and from Drosophila and
 CC C. elegans whole body cDNA preps. by PCR using the above primers.
 CC The DNA and deduced AA sequences of the resulting PCR fragments
 CC (including sequences corresp. to the PCR primers) are given in
 CC Q68971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison
 CC of the deduced AA sequences indicates a similarity, in particular,

CC there are three sets of clones that appear to be cross-species
 CC homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and
 CC HUMAN-11; and MOUSE-326 and HUMAN-42.
 SQ Sequence 43 AA;

Query Match 86.8%; Score 46; DB 11; Length 43;
 Best Local Similarity 83.3%; Pred. No. 7.66e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 yrlvir 16
 |||||
 QY 1 YRLLR 6

RESULT 6

ID R87142 standard; Peptide; 43 AA.
 AC R87142:
 DE 29-AUG-1996 (first entry)
 KW Protocadherin clone DROSOPHILA-12.
 KW Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse;
 OS catenin; therapy; clone; frog; fruit fly.
 OS Drosophila melanogaster.
 FH Key Location/Qualifiers
 FT Misc_difference 38
 FT /note= "encoded by CGA"
 FT Misc_difference 39
 FT /note= "encoded by ATG"
 FT Misc_difference 40
 FT /note= "encoded by ACA"
 FT Misc_difference 41
 FT /note= "encoded by ATG"
 FT Misc_difference 42
 FT /note= "encoded by CGC"
 FT Misc_difference 43
 FT /note= "encoded by CGC"
 PN WO9600289-A1.
 PD 04-JAN-1996.
 PF 26-JUN-1995; U08071.
 PR 27-JUN-1994; US-268161.
 PA (DOHE-) DOHENY EYE INST.
 PI Suzuki S;
 DR WPI; 96-068873/07.
 DR N-PSDB; T03617.
 DT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat
 PT pc5 - involved in cell-cell adhesion and regulation activities
 PS Example 2; Page 67-68; 146pp; English.
 CC R87142-R87144 represent partial fragments of the drosophila protocadherin
 CC sequence. The cDNAs encoding these sequences were isolated after
 CC screening a drosophila whole body cDNA preparation with the primers shown
 CC in T03575 and T03576. The primers were constructed from portions of the
 CC amino acid sequences of the third and fourth extracellular domains of
 CC published cadherin sequences. The cytoplasmic domain of cadherin
 CC interacts with the cytoskeleton through catenins and other cytoskeleton
 CC associated proteins. The cytoplasmic domain is not present in all
 CC cadherins, but in those which possess it, it is essential for the
 CC cadherins adhesive function. The cadherins which do not possess a
 CC cytoplasmic domain appear to function via a different method from those
 CC with a cytoplasmic domain. These protein sequences are involved in
 CC cell-cell adhesion. These sequences may have regulatory functions in the
 CC cell, as well as the cell-cell adhesive properties. Antibodies produced
 CC against these sequences are useful for modulating the binding activity of
 CC these protocadherins, and can be used therapeutically.
 SQ Sequence 43 AA;

Query Match 86.8%; Score 46; DB 17; Length 43;
 Best Local Similarity 83.3%; Pred. No. 7.66e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 yrlvir 16
 |||||
 QY 1 YRLLR 6

RESULT 7

ID R95698 standard; Protein; 434 AA.
 AC R95698:
 DE 20-SEP-1996 (first entry)
 KW Erythrocyte longus lycopene cyclase protein.
 KW Phytoene dehydrogenase; Erythrocyte longus; Erwinia hebicola; probe;
 KW open reading frame; lycopene cyclase; Rhodobacter sphaeroides;
 KW beta-carotene; food colourant; additive; anti-cancer.
 OS Erythrocyte longus.
 PN J0808241-A.
 PD 09-APR-1996.
 PF 30-SEP-1994; 236621.
 PR 30-SEP-1994; JP-236621.
 PA (ASAH) ASAH KASEI KOGYO KK.
 DR WPI; 96-233337/24.
 DR N-PSDB; T31799.
 DT Erythrocyte sp. phytoene dehydrogenase and lycopene cyclase genes
 PT - for the prodn. of beta-carotene useful as a food colourant
 PS Example 1; Page 6-7; 7pp; Japanese.
 CC Erythrocyte longus ATCC 14126. The corresp. gene was isolated from an
 CC E. longus genomic DNA library using a 1 kb fragment of the phytoene
 CC dehydrogenase gene from Erwinia hebicola as a probe. The probe isolated
 CC a nucleotide fragment which contained two open reading frames (ORF).
 CC ORF2 (1578 bp) encodes the phytoene dehydrogenase (T31798) whereas ORF1
 CC (1302 bp) encodes lycopene cyclase. The two ORFs were inserted into the
 CC plasmid pRK415 to generate pRKCD. This plasmid was transformed into
 CC Rhodobacter sphaeroides for prodn. of the proteins. The phytoene
 CC dehydrogenase and lycopene cyclase can be used to produce beta-carotene
 CC for use as a food colourant or as a food additive with anti-cancer
 CC effects.
 SQ Sequence 434 AA;

Query Match 84.9%; Score 45; DB 18; Length 434;
 Best Local Similarity 83.3%; Pred. No. 9.94e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 340 yrlvir 345
 |||||
 QY 1 YRLLR 6

RESULT 8

ID R97246 standard; Protein; 4472 AA.
 AC R97246:
 DE 07-JAN-1997 (first entry)
 KW Virulence gene cluster polypeptide product.
 KW Mutant; adaptation; virulence factor; identification; screening;
 KW vaccine; drugs; infection; treatment.
 OS Salmonella typhimurium.
 FH Key Location/Qualifiers
 ET Region
 FT /note= "All x's in this sequence correspond to
 FT termination codons in the virulence gene
 FT cluster sequence given in T09224."
 PN WO9617951-A2.
 PD 13-JUN-1996.
 PF 11-DEC-1995; G02875.
 PR 09-DEC-1994; GB-024921.
 PR 31-JAN-1995; GB-001881.
 PR 05-MAY-1995; GB-009239.
 PA (RPM-) RPMs TECHNOLOGY LTD.
 PI Holden DW;
 DR WPI; 96-287194/29.

Query Match 84.9%; Score 45; DB 18; Length 434;
 Best Local Similarity 83.3%; Pred. No. 9.94e+01;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 340 yrlvir 345
 |||||
 QY 1 YRLLR 6

CC marker sequence, or clones of the said microorganism; (2) providing
 CC individually a stored sample of each mutant produced by step (1) and
 CC providing individually stored nucleic acid comprising the unique
 CC marker sequence from each individual mutant; (3) introducing a
 CC plurality of mutants produced by step (1) into the said particular
 CC environment and allowing those microorganisms which are able to do so
 CC to grow in the said environment; (4) retrieving microorganisms from
 CC the said environment or a selected part thereof and isolating the
 CC nucleic acid from the retrieved microorganisms; (5) comparing any
 CC marker sequences in the nucleic acid isolated in step (4) to the
 CC unique marker sequence of each individual mutant stored as in step
 CC (2); and (6) selecting an individual mutant which does not contain any
 CC of the marker sequences as isolated in step (4). The products and
 CC methods can be used for identifying virulence genes in microorganisms.
 CC The mutant microorganisms can be used in vaccines or to screen for
 CC drugs which reduce virulence or compounds useful for preventing,
 CC ameliorating or treating infections in animals or plants.
 SQ Sequence 4472 AA;

Query Match 83.0%; Score 44; DB 19; Length 4472;
 Best Local Similarity 66.7%; Pred. No. 1.29e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 200 yrlmr 205
 |||:|
 Qy 1 YRLMR 6

RESULT 9
 ID R61548 standard; peptide; 10 AA.
 AC R61548;
 DT 11-MAY-1995 (first entry)
 DE Peptide fragment (1.0914) of HPV binds HLA-A2.1.
 KW antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
 KW HIV; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen.
 OS Human papilloma virus strain 18.
 PN WO9420127-A.
 PD 15-SEP-1994.
 PF 04-MAR-1994; U02353.
 PR 05-MAR-1993; US-027146.
 PR 04-JUN-1993; US-073205.
 PR 29-NOV-1993; US-159184.
 PA (CYTE-) CYTEL CORP.
 PI Grey HM, Kast WM, Sette A, Sidney J;
 DR WPI; 94-302678/37.
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 PS Example 5; Page 109; 138pp; English.
 CC R59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1
 CC binding motif. These peptides bind HLA-A2.1 and have a binding
 CC affinity of at least 1% as compared to a reference peptide (R71293).
 CC R61548 has an IC50 of 0.0036 and the sequence occurs at position 24
 CC in the HPV E6 protein. The peptides of the invention can induce
 CC cytotoxic T lymphocytes which can react with target cells. They can
 CC be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 SQ Sequence 10 AA;

Query Match 81.1%; Score 43; DB 11; Length 10;
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 3 yllmr 8
 |||:|
 Qy 1 YRLMR 6

RESULT 10
 ID R63866 standard; Protein; 158 AA.
 AC R63866;
 DT 28-JUN-1995 (first entry)
 DE HPV18 E6/E7 proteins.
 KW HPV; HPV18; E6 protein; E7 protein; diagnosis; cervical dysplasia;
 KW cervix cancer.
 OS Human papillomavirus strain 18.
 PN WO9426934-A.
 PD 24-NOV-1994.
 PF 06-MAY-1994; U05085.
 PR 06-MAY-1993; US-058920.
 PA (BAXT) BAXTER DIAGNOSTICS INC.
 PI Brown JT;
 DR WPI; 95-006821/01.
 DR P-PSDB; Q75471.
 PT Human papilloma virus detection assay - by amplification using
 PT self sustained sequence replication and hybridisation with a
 PT detector probe
 PS Disclosure; Page 27-28; 79pp; English.
 CC The sequences of the E6 and E7 polypeptide-encoding regions of human
 CC papillomavirus (HPV) 16 and 18 are given in Q75470-71 and the
 CC encoded proteins in R63865-66, respectively. Probes and primers
 CC based on these sequences were used for HPV infection diagnosis;
 CC expression of E6 and E7 is diagnostic for cervical cancer or pre-
 CC malignant states.
 SQ Sequence 158 AA;

Query Match 81.1%; Score 43; DB 12; Length 158;
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 99 yllmr 104
 |||:|
 Qy 1 YRLMR 6

RESULT 11
 ID R79656 standard; Protein; 158 AA.
 AC R79656;
 DT 06-DEC-1995 (first entry)
 DE HPV-18 E6 protein.
 KW Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell cycle;
 KW cell proliferation; cancer; psoriasis; fibrosis.
 OS Homo sapiens.
 PN WO9518974-A.
 PD 13-JUL-1995.
 PF 04-JAN-1995; U00164.
 PR 04-JAN-1994; US-176937.
 PR 23-MAY-1994; US-247904.
 PR 27-MAY-1994; US-250795.
 PR 13-SEP-1994; US-305520.
 PA (MITO-) MITOTIX INC.
 PI Cottarel G, Draetta G, Eckstein JW, Gyuris J, Rolfe M;
 DR WPI; 95-255137/33.
 DR N-PSDB; Q97848.
 PT Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle
 PT regulatory proteins - also new ubiquitin conjugating enzymes, their
 PT related nucleic acid, vectors, antibodies etc., useful for regulating
 PT e.g. cell proliferation
 PS Disclosure; Page 100-101; 157pp; English.
 CC HPV-18 E6 cDNA (given in Q97848) was amplified from a HeLa cell
 CC cDNA library using the primers given in Q97846-47. The gene
 CC was subcloned into a baculovirus vector for expression of
 CC recombinant E6 in Sf9 insect cells for use as a component of an
 CC in vitro ubiquitin conjugating system.
 SQ Sequence 158 AA;

Query Match 81.1%; Score 43; DB 14; Length 158;
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 99 yllmr 104

```

QY      1 YRLIIR 6
      1 | | | |
RESULT  12
ID R27728 standard; Protein; 271 AA.
AC R27728;
DT 09-MAR-1993 (first entry)
DE HPV 18 E6 protein fragment.
KW Virus vector; vaccinia virus; papillomavirus; HPV; human;
OS amplification; immunotherapeutic.
OS Human papillomavirus 18.
FH Key Location/Qualifiers
FT Peptide 2..259
FT /note="HPV-18 E6 protein"
PN W09216636-A.
PD 01-OCT-1992.
PF 10-MAR-1992; G00424.
PR 14-MAR-1991; GB-005383.
PA (IMMU ) IMMUNOLOGY LTD.
PI Boursnell MEG, Inglis SC, Munro AJ;
DR WPI; 92-349219/42.
DR N-PSDB; Q29390.
PT Recombinant virus vectors encoding human papillomavirus proteins
PT - for treating and vaccinating against HPV infections and
PT conditions caused by them, such as cervical cancer
PS Disclosure; Fig 1b; 83pp; English.
CC The fragment of DNA contg. the HPV-18 E6/E7 coding region was
CC prep'd. by PCR from plasmid pBR322/HPV16 (Boshart et al., EMBO J. 3:
CC 1151) using oligonucleotides S01 and S02. The prod. of the
CC second reading frame is the HPV-18 E7 protein whereas the third
CC reading frame encodes HPV-18 E6. The E6 and E7 ORFs are fused
CC together to form a single continuous ORF via site directed mutagenesis
CC and the immortalising potential of E7 is removed by altering two key
CC codons of the HPV E7 sequence. The single ORF of HPV-18 E6/E7 may be
CC inserted into vaccinia virus DNA at neutral sites (pref. by inserting
CC two sets of the DNA in opposite orientations to overcome the problem
CC of intertypic recombination) to make a recombinant virus vector for
CC use immunotherapeutically to activate cells of the immune system
CC against HPV. See also R27723-43.
SQ Sequence 271 AA;

Query Match 81.1%; Score 43; DB 5; Length 271;
Best Local Similarity 83.3%; Pred. No. 1.66e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 100 ynlir 105
      1 | | | |
QY      1 YRLIIR 6

RESULT  13
ID R27642 standard; Protein; 451 AA.
AC R27642;
DT 03-MAR-1993 (first entry)
DE Human calcium channel 27980/4.
KW Plasmid p1247-10.1.1.1; Ca-flux assay; SS.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc.difference 417
FT /note="encoded by GNN codon, N is unknown"
PN EP-507170-A.
PD 07-OCT-1992.
PF 23-MAR-1992; 104970.
PR 04-APR-1991; DE-110785.
PA (FARB ) BAYER AG.
PI Franz J, Rae P, Unterbeck A, Weingaertner B;
DR WPI; 92-333445/41.
DR P-PSDB; R27642.
PT Cloned human neuronal calcium channel sub-types - useful in
PT calcium flux assays to screen for neurone-specific calcium
PT channel ligands
PS Claim 2; Page 24-27; 101pp; German.

CC Human neuroblastoma cell line, hippocampus, frontal and temporal
CC cortex and visual cortex cDNA banks were screened with a probe
CC containing carp skeletal muscle ca-channel cDNA. The cDNA clone
CC p1247-10.1.1.1 was sequenced and found to encode amino acids 1050 to
CC 1512 including the end of the third domain (IIS6) and the entire
CC domain IV and about 130 C-terminal flanking amino acids which
CC correspond to the last cytoplasmic part of the protein. The human
CC neuronal calcium channel proteins can be used for screening for Ca
CC channel ligands (agonists or antagonists). See also Q29259-Q29275.
SQ Sequence 451 AA;

Query Match 81.1%; Score 43; DB 5; Length 451;
Best Local Similarity 86.7%; Pred. No. 1.66e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 380 ykllir 385
      1 | | | |
QY      1 YRLIIR 6

RESULT  14
ID R63808 standard; Protein; 652 AA.
AC R63808;
DT 28-JUN-1995 (first entry)
DE Human amphotropic retrovirus receptor GLVR2.
KW Amphotropic retrovirus receptor; gibbon leukemia virus receptor 2;
KW GLVR2; gene therapy.
OS Homo sapiens.
PN EP-622377-A.
PD 02-NOV-1994.
PF 28-MAR-1994; 104889.
PR 16-APR-1993; US-050584.
PA (AMCY ) AMERICAN CYANAMID CO.
PI Johann SV, Ohara BM, Van Zeijl M, O'hara BM;
DR WPI; 94-334580/42.
DR N-PSDB; Q74311.
PT Nucleic acid sequence encoding an amphotropic retrovirus receptor
PT - used to create viral vectors useful in gene therapy.
PS Claim 4; Fig 2; 24pp; English.
CC Q74311 encodes R63808 the amphotropic retrovirus receptor, gibbon
CC leukaemia virus receptor 2 (GLVR2). Nucleotide fragments of Q74311
CC can be used to create vectors, for use in human gene therapy and
CC for the transformation of host cells enabling them to express the
CC GLVR2 gene and receptor. The nucleotide fragments can also be used
CC as probes to study GLVR2 distribution in cells from various species
CC and tissues.
SQ Sequence 652 AA;

Query Match 81.1%; Score 43; DB 12; Length 652;
Best Local Similarity 83.3%; Pred. No. 1.66e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 377 yrlir 382
      1 | | | |
QY      1 YRLIIR 6

RESULT  15
ID R32925 standard; Protein; 1592 AA.
AC R32925;
DT 28-JUN-1993 (first entry)
DE Glucosyltransferase I.
KW GT-I; Streptococcus; Dental; caries.
OS Streptococcus sobrinus.
PN J05023188-A.
PD 02-FEB-1993.
PF 25-JUL-1991; 186592.
PR 25-JUL-1991; JP-186592.
PA (FUKU/) FUKUI I.
PA (KATO/) KATO K.
DR WPI; 93-079449/10.
DR N-PSDB; Q37760.
PT DNA sequence glucosyl:transferase-I - comprises Streptococcus

```

PT sobrinus DNA sequence with at least one nucleotide added or
 PT deleted
 PS Claim 13; Page 15; 29pp; Japanese.
 CC The DNA sequence from Streptococcus sobrinus strain 6715 encodes
 CC glucosyltransferase-I (and mutants). The DNA was obtd. by treating
 CC S. sobrinus 6715 with mutanolysin, extracting the chromosomal DNA,
 CC partially digesting with Sau3AI and fractionating on agarose gel.
 CC The 3-5 kbp fragment was ligated into pUC18 and E. coli JM109
 CC transformed with it. A GT-1 expressing clone was isolated and
 CC sequenced. The clone may be used in the development of a drug for
 CC dental caries.
 SQ Sequence 1592 AA;

Query Match 81.1%; Score 43; DB 6; Length 1592;
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 371 yrllnr 376
 |||||
 QY 1 YRLILR 6

Search completed: Thu May 22 08:30:51 1997
 Job time : 16 secs.

```

> O <
O I O IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq2" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "seq2.key": SEQ 10 NO. 2
seq2 (AA) ID seq2 AA preliminary pattern
1 followed by
2 any character
2 g or r
2 r or l
2 any character
2 i or n
2 r or g
2 l
2 d or s or n
2 e or v
2 r

Selected data banks and files:

Data bank : A-GeneSeq 26, all entries
Data bank : PIR 50, all entries
Data bank : Swiss-Prot 34, all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact File Options:
Find non-matching hits only No Indirect file
Report key used Yes Sequence or key file
List of hits Yes
Note position of hit Yes
Hit display Yes
Display full annotations Yes
Name and annotations Yes
Sequence context 10

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

-----
1 match found in sequence:
R92909 : HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
(from "A-GeneSeq 26")
ID R92909 standard; peptide; 20 AA.
AC R92909;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequence
is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
HLA-B2702. These sequences can be used to extend the period of
acceptance by a recipient of a transplant from an MHC unmatched donor.
The peptides are administered to a patient in conjunction with a
subtherapeutic amount of an immunosuppressant. This is administered to
the patient for a limited period of time (compared to the lifetime
administration for current treatments). The peptides particularly
modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 1 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 1 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

-----
1 match found in sequence:
R92913 : HLA-B7 CTL modulating peptide (B7.84-75/75-84).
(from "A-GeneSeq 26")
ID R92913 standard; peptide; 20 AA.
AC R92913;
DT 16-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.84-75/75-84).

```

```

CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 1 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 1 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

-----
1 yrlairlnerrlnrtalry
1 10
...

-----
2 matches found in sequence:
R92911 : HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
(from "A-GeneSeq 26")
ID R92911 standard; peptide; 20 AA.
AC R92911;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequence
is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
HLA-B2702. These sequences can be used to extend the period of
acceptance by a recipient of a transplant from an MHC unmatched donor.
The peptides are administered to a patient in conjunction with a
subtherapeutic amount of an immunosuppressant. This is administered to
the patient for a limited period of time (compared to the lifetime
administration for current treatments). The peptides particularly
modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

-----
1 yrlairlnerrlnrtalry
1 10 20
...

-----
1 match found in sequence:
R92913 : HLA-B7 CTL modulating peptide (B7.84-75/75-84).
(from "A-GeneSeq 26")
ID R92913 standard; peptide; 20 AA.
AC R92913;
DT 16-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.84-75/75-84).

```

```

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B7.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B/5-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B7. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 0 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Q; 2 E; 0 Z; 2 G; 0 H;
SQ 0 I; 4 L; 0 K; 0 M; 0 F; 0 P; 2 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

1 ygrlnrlsrreslnlrgy
1 10
...
1 match found in sequence:
R92907 ; HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
(from "A-Geneseq 26")
ID R92907 standard; peptide; 20 AA.
AC R92907;
AT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B/5-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

```

```

SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

1 yrlairlnherrenlrialry
1 10
...
1 match found in sequence:
R95428 ; HLA-B2702 84-75-84 palindrome.
(from "A-Geneseq 26")
ID R95428 standard; peptide; 20 AA.
AC R95428;
AT 12-NOV-1996 (first entry)
DE HLA-B2702 84-75-84 palindrome.
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PR 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

1 yrlairlnherrenlrialry
1 10
...
1 match found in sequence:
R95415 ; HLA-B7.84-75-84 Palindrome.
(from "A-Geneseq 26")
ID R95415 standard; peptide; 20 AA.
AC R95415;
AT 12-NOV-1996 (first entry)
DE HLA-B7.84-75-84 Palindrome.
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

```

KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STUD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 18; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. These sequences can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 20 AA;
SQ 0 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 2 G; 0 H;
SQ 0 I; 4 L; 0 K; 0 M; 0 F; 0 P; 2 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

1 ygrlnrlserreslnlrgy
10

-- Search Statistics --

| | | |
|--------------------------------|-------------|---------------|
| Times: | CPU | Total Elapsed |
| | 00:07:08.00 | 00:07:13.00 |
| Number of sequences searched: | | 241556 |
| Number of sequence hits: | | 6 |
| Number of separate matches: | | 7 |
| Number of sequence hits saved: | | 0 |

THIS PAGE BLANK (USPTO)

WPSORCH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:48:41 1997; MasPar time 2.83 Seconds
201.600 Million cell updates/sec
Tabular output not generated.

Title: >US-08-653-294-31
Description: (1-20) from US08653294.pep
Perfect Score: 154
Sequence: 1 YRLAIRLNERYLRLAIRLNER 20

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 28.882; Variance 64.246; scale 0.450

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Score | Match | Length | DB | ID | Description | Pred. No. |
|--------|-------|-------|--------|----|----|-------------|-----------|
|--------|-------|-------|--------|----|----|-------------|-----------|

No matches found.

Search completed: Thu May 22 08:49:00 1997
Job time : 19 secs.

THIS PAGE BLANK (USPTO)

WPIRLH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:48:13 1997; MasPar time 2.10 Seconds
Tabular output not generated. 202.262 Million cell updates/sec

Title: >US-08-653-294-31
Description: (1-20) from US08653294.pep
Perfect Score: 154
Sequence: 1 YRLAIRLNERYLRLAIRLNER 20

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: swiss-prot34
1:part1 2:part3 3:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 30.299; Variance 54.375; scale 0.557

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

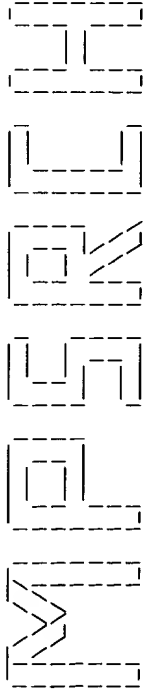
SUMMARIES

| Result | Query | | | | |
|-----------|-------|-------|--------|----|-------------|
| No. | Score | Match | Length | ID | Description |
| Pred. No. | | | | | |

No matches found.

Search completed: Thu May 22 08:48:23 1997
Job time : 10 secs.

THIS PAGE BLANK (USPTO)



Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:49:18 1997; MasPar time 1.99 Seconds
Tabular output not generated. 109.404 Million cell updates/sec

Title: >US-08-653-294-31
Description: (1-20) from US08653294.pep
Perfect Score: 154
Sequence: 1 YRLAIRLNERVRLAIRLNER 20

Scoring table: PAM 150
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: a-geneseq26

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 19.740; Variance 84.009; scale 0.235

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|-----------------------|-----------|
| 1 | 154 | 100.0 | 20 16 | R92911 | HLA-B2702 CTL modul | 6.55e-07 |
| 2 | 83 | 53.9 | 20 18 | R95428 | HLA-B2702 84-75-84 pa | 1.33e+00 |
| 3 | 83 | 53.9 | 20 16 | R92907 | HLA-B2702 CTL modul | 1.33e+00 |
| 4 | 78 | 50.6 | 20 16 | R92909 | HLA-B2702 CTL modul | 3.49e+00 |
| 5 | 76 | 49.4 | 20 16 | R92908 | HLA-B2702 CTL modul | 5.10e+00 |
| 6 | 72 | 46.8 | 20 18 | R95430 | HLA-B2702 84-75/75-8 | 1.09e+01 |
| 7 | 71 | 46.1 | 20 16 | R92910 | HLA-B2702 CTL modul | 1.31e+01 |

Note: Post-processor removed 38 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID R92911 standard; peptide; 20 AA.
AC R92911;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
Query Match 100.0%; Score 154; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.55e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 yrlairlneryrlairlnr 20
QY 1 YRLAIRLNERVRLAIRLNER 20
RESULT 2
ID R95428 standard; peptide; 20 AA.
AC R95428;
DT 12-NOV-1996 (first entry)
DE HLA-B2702 84-75-84 palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW Cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702 60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 18; Length 20;
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Db 1 yrlairlner-renlralr 19
 ||||| ||||| :| :|
 QY 1 YRLAIRLNERYLRLAIRLNER 20

RESULT 3

ID R92907 standard; peptide; 20 AA.

AC R92907;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 class I major histocompatibility complex (MHC) antigens. This sequence
 is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 I MHC HLA-B2702. These sequences can be used to extend the period of
 acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 subtherapeutic amount of an immunosuppressant. This is administered to
 the patient for a limited period of time (compared to the lifetime
 administration for current treatments). The peptides particularly
 modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 of the patient.
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 16; Length 20;
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Db 1 yrlairlner-renlralr 19
 ||||| ||||| :| :|
 QY 1 YRLAIRLNERYLRLAIRLNER 20

RESULT 4

ID R92909 standard; peptide; 20 AA.

AC R92909;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 class I major histocompatibility complex (MHC) antigens. This sequence
 is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 I MHC HLA-B2702. These sequences can be used to extend the period of
 acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 subtherapeutic amount of an immunosuppressant. This is administered to
 the patient for a limited period of time (compared to the lifetime
 administration for current treatments). The peptides particularly
 modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 of the patient.
 SQ Sequence 20 AA;

Query Match 50.6%; Score 78; DB 16; Length 20;
 Best Local Similarity 65.0%; Pred. No. 3.49e+00;
 Matches 13; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 1 yrlairlner-renlralr 19
 ||||| ||||| :| :|
 QY 1 YRLAIRLNERYLRLAIRLNER 20

RESULT 5

ID R92908 standard; peptide; 20 AA.

AC R92908;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 class I major histocompatibility complex (MHC) antigens. This sequence
 is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 I MHC HLA-B2702. These sequences can be used to extend the period of
 acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 subtherapeutic amount of an immunosuppressant. This is administered to
 the patient for a limited period of time (compared to the lifetime
 administration for current treatments). The peptides particularly
 modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 of the patient.
 SQ Sequence 20 AA;

Query Match 49.4%; Score 76; DB 16; Length 20;
 Best Local Similarity 60.0%; Pred. No. 5.10e+00;
 Matches 12; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 1 yrlairlner-renlralr 19
 ||||| ||||| :| :|
 QY 1 YRLAIRLNERYLRLAIRLNER 20

RESULT 6

ID R95430 standard; peptide; 20 AA.

AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75T/75-84T palindrome.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;

KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW Cytolysis; antigen presenting cell.
 OS Synthetic.

PN W09513288-A1.

PD 18-MAY-1995.

PR 10-NOV-1994; U12985.

PF 10-NOV-1993; US-150493.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM;

DR WPI; 95-194027/25.

PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 12; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B*2702 84-75T/75-84T palindromic. These sequences can be used to
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B*2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B*2702 60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.

CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 46.8%; Score 72; DB 18; Length 20;

Best Local Similarity 72.2%; Pred. No. 1.09e+01;

Matches 13; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 1 Yrlairlnetrenlrtrial 18

QY 1 YRLAIRLINE-RYRLAIRL 17

RESULT 7

ID R92910 standard; peptide; 20 AA.

AC R92910;

DT 16-MAY-1996 (first entry)

DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW class I MHC; HLA-B*2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B*75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha 1 domain of the class
 CC I MHC HLA-B*2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.

SQ Sequence 20 AA;

Query Match 46.1%;

Best Local Similarity 60.0%; Score 71; DB 16; Length 20;

Matches 12; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

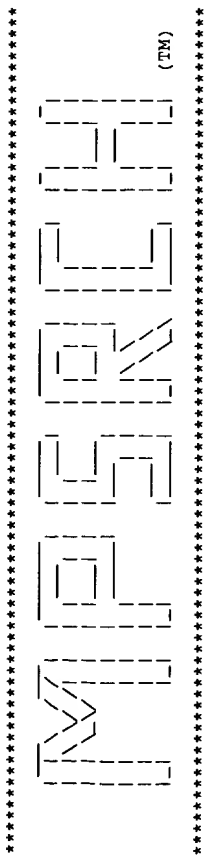
Db 1 Yrlairlnetrenlrtrial 19

QY 1 YRLAIRLINE-RYRLAIRL 20

Search completed: Thu May 22 08:49:27 1997

Job time : 9 secs.

THIS PAGE BLANK (USPTO)



Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 08:47:21 1997; MasPar time 2.92 Seconds
195.000 Million cell updates/sec
Tabular output not generated.

Title: >US-08-653-294-26
Description: (1-20) from US08653294.pep
Perfect Score: 154
Sequence: 1 YRLAIRLNERRENLRALRY 20

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: pir50
1:unnn1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 30.116; Variance 61.232; scale 0.492

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | No. | Score | Match | Length | DB | ID | Description | Pred. No. |
|--------|-------|-------|-------|-------|--------|-------|-------|-------------|-----------|
| ----- | ----- | ----- | ----- | ----- | ----- | ----- | ----- | ----- | ----- |

No matches found.

Search completed: Thu May 22 08:47:32 1997
Job time : 11 secs.

THIS PAGE BLANK (USPTO)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

Run on: Thu May 22 08:46:58 1997; MasPar time 2.04 Seconds

Tabular output not generated. 207.603 Million cell updates/sec

Title: >US-08-653-294-26
Description: (1-20) from US08653294.pep
Perfect Score: 154
Sequence: 1 YRLAIRLNERRENRLRY 20

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 31.472; Variance 50.872; scale 0.619

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | No. | Score | Match | Length | DB | ID | Description | Pred. No. |
|--------|-------|-----|-------|-------|--------|----|----|-------------|-----------|
| ----- | | | | | | | | | |

No matches found.

Search completed: Thu May 22 08:47:04 1997
Job time : 6 secs.

THIS PAGE BLANK (USPTO)

immunosuppressant; graft versus host disorder; transplantation; therapy;
 class I MHC; HLA-B2702.
 Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 100.0%; Score 154; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.21e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YRLAIRLNERENLRALRY 20
 QY 1 YRLAIRLNERENLRALRY 20

RESULT 3
 ID R92909 standard; peptide; 20 AA.
 AC R92909;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 95.5%; Score 147; DB 16; Length 20;
 Best Local Similarity 95.0%; Pred. No. 6.09e-07;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIRLNERENLRALRY 20
 QY 1 YRLAIRLNERENLRALRY 20

RESULT 4
 ID R92908 standard; peptide; 20 AA.
 AC R92908;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 CC Sequence 20 AA;

Query Match 95.5%; Score 147; DB 16; Length 20;
 Best Local Similarity 95.0%; Pred. No. 6.09e-07;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIRLNERENLRALRY 20
 QY 1 YRLAIRLNERENLRALRY 20

RESULT 5
 ID R92910 standard; peptide; 20 AA.
 AC R92910;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
 CC I MHC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 90.9%; Score 140; DB 16; Length 20;
 Best Local Similarity 90.0%; Pred. No. 3.05e-06;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 YRLAIRLNERRLRLALRY 20
 QY 1 YRLAIRLNERRLRLALRY 20

RESULT 6

ID R95430 standard; peptide; 20 AA.
 AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75T/75-84T palindromic.
 KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25

PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75T/75-84T palindromic. These sequences can be used to
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.
 CC Candidate compounds can be screened for their effect on the cytolytic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;

Query Match 85.1%; Score 131; DB 18; Length 20;
 Best Local Similarity 94.7%; Pred. No. 2.39e-05;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIRLNERRLRLALRY 19
 QY 1 YRLAIRLNERRLRLALRY 19

RESULT 7

ID R92911 standard; peptide; 20 AA.
 AC R92911;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.

PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 16; Length 20;
 Best Local Similarity 65.0%; Pred. No. 9.02e-01;
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Db 1 YRLAIRLNERRLRLALRY 20
 QY 1 YRLAIRLNERRLRLALRY 19

RESULT 8

ID R83062 standard; peptide; 10 AA.
 AC R83062;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.75-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.

OS Synthetic.
 PN WO9526979-A1.
 PD 12-OCT-1995.
 PR 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host

PS Claim 15; Page 9; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialy 10
 QY 11 RENLRIALRY 20
 RESULT 9
 ID R95413 standard; peptide; 10 AA.
 AC R95413;
 DT 12-NOV-1996 (first entry)
 DE Alpha1-helix of HLA-B2702.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compans. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11: 29pp; English.
 CC This sequence represents the alpha1-helix of the
 CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;
 Query Match 50.0%; Score 77; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 renltrialy 10
 QY 11 RENLRIALRY 20
 RESULT 10
 ID R41208 standard; peptide; 10 AA.
 AC R41208;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN W09317699-A.
 PD 16-SEP-1993.
 PR 25-FEB-1993; U01758.
 PF 02-MAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI; 93-303134/38.
 PT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets

PS Claim 11; Page 54; 61pp; English.
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
 CC activity, either by inhibition or stimulation. It can be used
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 CC This peptide sequence is more commonly found within larger peptide
 CC compounds of not more than 30 amino acids in length.
 SQ Sequence 10 AA;
 Query Match 50.0%; Score 77; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 renltrialy 10
 QY 11 RENLRIALRY 20
 RESULT 11
 ID R92912 standard; peptide; 15 AA.
 AC R92912;
 DT 16-MAY-1996 (first entry)
 DE HLA-B2702 CTL modulating peptide (B2702.70-84).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW class I MHC; HLA-B2702.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349
 PR 05-APR-1994; US-222851.
 PI (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI; 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient
 PT host
 PS Example 15; Page 36; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R83097-R83093 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC
 CC HLA-B2702. These sequences can be used to extend the period of
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.
 CC The peptides are administered to a patient in conjunction with a
 CC subtherapeutic amount of an immunosuppressant. This is administered to
 CC the patient for a limited period of time (compared to the lifetime
 CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 15 AA;
 Query Match 50.0%; Score 77; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 renltrialy 15
 QY 11 RENLRIALRY 20
 RESULT 12
 ID R95422 standard; peptide; 25 AA.
 AC R95422;
 DT 12-NOV-1996 (first entry)
 DE HLAB38.6084.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.

18-MAY-1995.
 10-NOV-1994; U12985.
 10-NOV-1993; US-150493.
 (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLAB38.6084. These sequences can be used to isolate the protein p74 from
 CC a T-cell lysate. p74 is a T-cell surface membrane protein associated
 CC with T-cell activation in mammalian T-cells, and is also immunologically
 CC cross reactive with the heat shock protein Hsc70. p74 is found in a
 CC limited number of cell types, but is particularly expressed on B and T
 CC cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renlrialry 25
 QY 11 RENLRIALRY 20
 |||||

RESULT 13

ID R95416 standard; peptide; 25 AA.
 AC R95416;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702.60-84.
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN W09513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compens. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 9; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents
 CC HLAB38.6084. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC this sequence, induces calcium influx, and inhibits cytotoxic T
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can

CC be screened for their effect on the cytolytic activity of T-cells, by
 CC combining them with the extracellular portion of p74 and determining the
 CC amount of binding between the candidate compound and p74. Modulation of
 CC CTL activity can be inhibited in a cellular composition containing
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the
 CC extracellular portion of p74, in an amount sufficient to compete with p74
 CC for the binding of the p74 ligand.
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renlrialry 25
 QY 11 RENLRIALRY 20
 |||||

RESULT 14

ID R41205 standard; peptide; 25 AA.
 AC R41205;
 DT 15-MAR-1994 (first entry)
 DE Peptide fragment of Class I HLA peptide.
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
 KW parasitic disease; cytotoxic T lymphocyte; modulation.
 OS Synthetic.
 PN W09317599-A.
 PD 16-SEP-1993.
 PF 25-FEB-1993; U01758.
 PR 02-NAR-1992; US-844716.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger CA, Krensky AM;
 DR WPI: 93-303134/38.
 DT New peptide(s) based on Class I HLA antigen domains - used for
 PT modulating cytotoxic T-lymphocyte activity towards targets
 PS Claim 8; Page 53; 61pp; English.
 CC The peptide (or a fragment of at least 10 amino acids, joined at at
 CC least one terminus to a sequence other than that of wild type HLA
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
 CC either by inhibition or stimulation. It can be used for
 CC inhibiting CTL toxicity in transplantations, for inducing CTL
 CC activity in parasitic diseases and neoplasia and in studies on viral
 CC infection. The peptide can also be used for identifying CTLs which
 CC bind to it and removing subsets of CTLs from a T-cell composition.
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renlrialry 25
 QY 11 RENLRIALRY 20
 |||||

RESULT 15

ID R83093 standard; peptide; 25 AA.
 AC R83093;
 DT 16-MAY-1996 (first entry)
 DE HLAB38 CTL modulating peptide (B38.6084).
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;
 KW Class I MHC; HLAB38.
 OS Synthetic.
 PN W09526979-A1.
 PD 12-OCT-1995.
 PF 05-APR-1995; U04349.
 PR 05-APR-1994; US-222851.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM, Parham P;
 DR WPI: 95-358582/46.
 PT Extension of acceptance period of transplants from MHC unmatched
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host
 PS Example 13; Page 32; 80pp; English.
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
 CC class I major histocompatibility complex (MHC) antigens. This sequence
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
 CC HLAB38. These sequences can be used to extend the period of acceptance
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides
 CC are administered to a patient in conjunction with a subtherapeutic amount
 CC of an immunosuppressant. This is administered to the patient for a
 CC limited period of time (compared to the lifetime administration for
 CC current treatments). The peptides particularly modulate (or inhibit) the
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred.No. 3.13e+00;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renlrialry 25
 |||||
 QY 11 RENLRIALRY 20

Search completed: Thu May 22 08:47:56 1997
 Job time : 6 secs.

> O <
O I O Intelligenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq1" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence. "seq1.key": **SEQ 10 No. 1**
Selected sequence key from "seq1.key":
seq1 (AA) ID seq1 AA preliminary pattern
followed by

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155
2156
2157
2158
2159
2160
2161
2162
2163
2164
2165
2166
2167
2168
2169
2170
2171
2172
2173
2174
2175
2176
2177
2178

```

SQ Sequence 366 AA;
SQ 38 A; 30 R; 5 N; 19 D; 0 B; 8 C; 21 Q; 28 E; 0 Z; 29 G; 9 H;
SQ 9 I; 30 L; 10 K; 6 M; 7 F; 18 P; 27 S; 24 T; 12 W; 13 Y; 23 V;
Found using 'seq1' (seq1.key)
...
89 qkykrqagdrvslnrlrgyynqseagsh
108
1 match found in sequence:
R12466 ; HLA-C exon Cb-2.
(from "A-GeneSeq 26")
AC R12466;
DE HLA-C exon Cb-2.
DE Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I.
OS Homo sapiens.
PN J03112485-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247695.
PR 22-SEP-1989; JP-247695.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182989/25.
DR N-PSDB; Q12117.
PT HLA-C gene, DNA probe and transformant cells - for immunisation
PT of animals and monoclonal antibody development.
PS Claim 4; Page 2; 13pp; Japanese.
CC Probes comprising part of the DNA sequence encoding the protein can
CC be used to identify Class I genes. The DNA can be expressed for
CC immunisation of animals and prodn. of monoclonal antibodies specific
CC for the HLA-C antigen. See also R12465 (same patent) and J03112485
CC and J03112487.
SQ Sequence 366 AA;
SQ 40 A; 32 R; 5 N; 20 D; 0 B; 9 C; 19 Q; 29 E; 0 Z; 29 G; 9 H;
SQ 9 I; 30 L; 10 K; 6 M; 6 F; 18 P; 22 S; 24 T; 11 W; 15 Y; 23 V;
Found using 'seq1' (seq1.key)
...
89 qkykrqagdrvslnrlrgyynhreaagst
108
1 match found in sequence:
R12463 ; HLA-Bw53 exon.
(from "A-GeneSeq 26")
ID R12463 standard; Protein; 362 AA.
AC R12463;
DE HLA-Bw53 exon.
DE Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I.
OS Homo sapiens.
PN J03112487-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR N-PSDB; Q12114.
PT HLA-Bw53 gene, DNA probe and transformant cells - used for
PT immunisation, identifying specificity of antiserum etc.
PS Claim 2; Page 1; 11pp; Japanese.

```

```

CC Probes comprising part of the sequence encoding the protein can be
CC used to identify Class I genes. The DNA can be expressed for
CC immunisation of animals and prodn. of monoclonal antibodies
CC specific for the HLA-Bw53 antigen. See also J03112485 and
CC J03112486.
SQ Sequence 362 AA;
SQ 38 A; 29 R; 5 N; 20 D; 0 B; 5 C; 21 Q; 24 E; 0 Z; 27 G; 8 H;
SQ 13 I; 29 L; 9 K; 6 M; 7 F; 18 P; 24 S; 29 T; 11 W; 15 Y; 23 V;
SQ 0 Others;
Found using 'seq1' (seq1.key)
...
89 qifkntqtyrenlrlrgyynqseagsh
108
1 match found in sequence:
R12464 ; HLA-B35 antigen.
(from "A-GeneSeq 26")
ID R12464 standard; Protein; 362 AA.
AC R12464;
DE 29-AUG-1991 (first entry)
DE HLA-B35 antigen.
DE Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I.
OS Homo sapiens.
PN J03112486-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR N-PSDB; Q12115.
PT HLA-B35 gene - used in DNA probe and transformant cells for
PT immunising animals, for developing monoclonal antibody.
PS Claim 1; Page 1; 11pp; Japanese.
CC Probes comprising part of the sequence encoding this sequence can
CC be used to identify Class I genes. The DNA can be expressed for
CC immunisation of animals and prodn. of monoclonal antibodies
CC specific for the HLA-B35 antigen. See also J03112485 and J03112487.
SQ Sequence 362 AA;
SQ 37 A; 29 R; 6 N; 20 D; 0 B; 5 C; 21 Q; 24 E; 0 Z; 28 G; 8 H;
SQ 12 I; 29 L; 9 K; 5 M; 7 F; 18 P; 25 S; 29 T; 11 W; 15 Y; 24 V;
Found using 'seq1' (seq1.key)
...
89 qifkntqtyreslnrlrgyynqseagsh
108
1 match found in sequence:
R41205 ; Peptide fragment of Class I HLA peptide.
(from "A-GeneSeq 26")
ID R41205 standard; peptide; 25 AA.
AC R41205;
DE 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
DE Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.

```

```

PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 8; Page 53; 61pp; English.
CC The peptide (or a fragment of at least 10 amino acids, joined at at
CC least one terminus to a sequence other than that of wild type HLA
CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
CC either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
SQ Sequence 25 AA;
SQ 3 A; 4 R; 1 N; 2 D; 0 B; 1 C; 2 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 2 K; 0 M; 0 F; 0 P; 0 S; 2 T; 1 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

...

6 qickakagtrenlrly 25
|------|
16 renlrly 10

-----
1 match found in sequence:
R41206 ; Peptide fragment of Class I HLA peptide.
(from "A-Geneseq 26")
ID R41206 standard; peptide; 25 AA.
AC R41206;
DE 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
DE Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 9; Page 53; 61pp; English.
CC The peptide (or a fragment of at least 10 amino acids, joined at at
CC least one terminus to a sequence other than that of wild type HLA
CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
CC either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
SQ Sequence 25 AA;
SQ 1 A; 5 R; 1 N; 2 D; 0 B; 0 C; 3 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 2 Y; 1 V;
Found using 'seq1' (seq1.key)

...

6 qkykrqagtdrvlnlrly 25
|------|
16 renlrly 10

-----
1 match found in sequence:
R41207 ; Peptide fragment of Class I HLA peptide.
(from "A-Geneseq 26")
ID R41207 standard; peptide; 25 AA.
AC R41207;
DE 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
DE Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW

```

```

KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 10; Page 54; 61pp; English.
CC The peptide (or a fragment of at least 10 amino acids, joined at at
CC least one terminus to a sequence other than that of wild type HLA
CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,
CC either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
SQ Sequence 25 AA;
SQ 0 A; 4 R; 2 N; 1 D; 0 B; 0 C; 2 Q; 2 E; 0 Z; 1 G; 0 H;
SQ 1 I; 2 L; 1 K; 0 M; 0 F; 0 P; 2 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

...

6 qiskntqtyreslnlrly 25
|------|
16 renlrly 10

-----
1 match found in sequence:
R41208 ; Peptide fragment of Class I HLA peptide.
(from "A-Geneseq 26")
ID R41208 standard; peptide; 10 AA.
AC R41208;
DE 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
DE Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 11; Page 54; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used
CC for inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide sequence is more commonly found within larger peptide
CC compounds of not more than 30 amino acids in length.
SQ Sequence 10 AA;
SQ 1 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

...

1 renlrly 10
|------|
1 renlrly 10

-----
1 match found in sequence:
R41209 ; Peptide fragment of Class I HLA peptide.
(from "A-Geneseq 26")

```

```

ID R41209 standard; peptide; 10 AA.
AC R41209;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 11; Page 54; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used
CC for inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide sequence is more commonly found within larger peptide
CC compounds of not more than 30 amino acids in length.
SQ Sequence 10 AA;
SQ 0 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 0 K; 0 M; 0 F; 0 P; 1 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

1 |-----|
  | reslnlrgy
  | 1
  | 10

-----
1 match found in sequence:
R48286 ; Peptide fragment of HLA-B38 antigen.
(from "A-GeneSeq 26")
ID R48286 standard; peptide; 25 AA.
AC R48286;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of HLA-B38 antigen.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Example 13; Page 39; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide is derived from the HLA-B38 antigen and corresponds
CC to the amino acid positions 60-84 of that antigen.
SQ Sequence 25 AA;
SQ 1 A; 4 R; 3 N; 1 D; 0 B; 1 C; 2 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

...
|-----|
| qickntqtyrenlialry
| 16
| 25

-----
1 match found in sequence:
R3061 ; HLA-B7 CTL modulating peptide (B7.75-84).
(from "A-GeneSeq 26")
ID R3061 standard; peptide; 10 AA.
AC R3061;
DT 15-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B7.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PS Claim 13; Page 66; 80pp; English.
CC This sequence represents a fragment of a class I major histocompatibility
CC complex (MHC) antigen. This sequence corresponds to residues 75-84 of
CC the alpha-1 domain of the class I MHC HLA-B7. This sequence, and the
CC peptide fragments represented by R3062-R3085, R3090-R3096 and
CC R92907-R92913 can be used to extend the period of acceptance by a
CC recipient of a transplant from an MHC unmatched donor. The peptides are
CC administered to a patient in conjunction with a subtherapeutic amount of
CC an immunosuppressant. This is administered to the patient for a limited
CC period of time (compared to the lifetime administration for current
CC treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 10 AA;
SQ 0 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 0 K; 0 M; 0 F; 0 P; 1 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

1 |-----|
  | reslnlrgy
  | 1
  | 10

-----
1 match found in sequence:
R3062 ; HLA-B2702 CTL modulating peptide (B2702.75-84).
(from "A-GeneSeq 26")
ID R3062 standard; peptide; 10 AA.
AC R3062;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PS Claim 15; Page 9; 80pp; English.
CC R3061-R3085, R3090-R3096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a

```

```

CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA;
SQ 1 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

|-----|
1 renlralry
10

-----
1 match found in sequence:
R92912 : HLA-B*2702 CTL modulating peptide (B2702.70-84).
(from "A-GeneSeq 26")
ID R92912 standard; peptide; 15 AA.
AC R92912;
DT 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.70-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
PT host
Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 15 AA;
SQ 2 A; 3 R; 1 N; 1 D; 0 B; 0 C; 1 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 1 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

|-----|
1 kaqtrenlralry
15
6

-----
1 match found in sequence:
R92913 : HLA-B*7 CTL modulating peptide (B7.84-75/75-84).
(from "A-GeneSeq 26")
ID R92913 standard; peptide; 20 AA.
AC R92913;
DT 16-MAY-1996 (first entry)
DE HLA-B*7 CTL modulating peptide (B7.84-75/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*7.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.

```

```

PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
PT host
Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*7. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 0 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 2 G; 0 H;
SQ 0 I; 4 L; 0 K; 0 M; 0 F; 0 P; 2 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

|-----|
1 ygrlnrlsrreslnrlrgy
11
20

-----
1 match found in sequence:
R83072 : HLA-B*46 CTL modulating peptide (Bw46.60-84).
(from "A-GeneSeq 26")
ID R83072 standard; peptide; 25 AA.
AC R83072;
DT 16-MAY-1996 (first entry)
DE HLA-B*46 CTL modulating peptide (Bw46.60-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*46.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
PT host
Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class
CC I MHC HLA-B*46. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 25 AA;
SQ 1 A; 5 R; 1 N; 2 D; 0 B; 0 C; 3 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 2 Y; 1 V;
Found using 'seq1' (seq1.key)

...

|-----|
6 qkykrqaqtdrvslrnlrgy
16
25

```

```

1 match found in sequence:
R83073 ; HLA-Bw62 CTL modulating peptide (Bw62.60-84).
  (from "A-Geneseq 26")
ID R83073 standard; peptide; 25 AA.
AC R83073;
DT 16-MAY-1996 (first entry)
DE HLA-Bw62 CTL modulating peptide (Bw62.60-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-Bw62.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLA-Bw62. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 25 AA;
SQ 0 A; 4 R; 2 N; 1 D; 0 B; 0 C; 2 Q; 2 E; 0 Z; 1 G; 0 H;
SQ 1 I; 2 L; 1 K; 0 M; 0 F; 0 P; 2 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

...

6 qiskntqttyreslnrly 16
  |-----|
  qickakagtddrenlrly 25

-----
1 match found in sequence:
R83090 ; HLA-B2702 CTL modulating peptide (B2702.60-84).
  (from "A-Geneseq 26")
ID R83090 standard; peptide; 25 AA.
AC R83090;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.60-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 25 AA;
SQ 1 A; 4 R; 3 N; 1 D; 0 B; 1 C; 2 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

...

6 qickntqttyrenlrly 16
  |-----|
  qickakagtddrenlrly 25

-----
1 match found in sequence:
R83094 ; HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
  (from "A-Geneseq 26")
ID R83094 standard; peptide; 10 AA.
AC R83094;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.

```

```

CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 25 AA;
SQ 3 A; 4 R; 1 N; 2 D; 0 B; 1 C; 2 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 2 K; 0 M; 0 F; 0 P; 0 S; 2 T; 1 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

...

6 qickakagtddrenlrly 16
  |-----|
  qickakagtddrenlrly 25

-----
1 match found in sequence:
R83093 ; HLAB38 CTL modulating peptide (B38.6084).
  (from "A-Geneseq 26")
ID R83093 standard; peptide; 25 AA.
AC R83093;
DT 16-MAY-1996 (first entry)
DE HLAB38 CTL modulating peptide (B38.6084).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLAB38.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLAB38. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 25 AA;
SQ 1 A; 4 R; 3 N; 1 D; 0 B; 1 C; 2 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

...

6 qickntqttyrenlrly 16
  |-----|
  qickakagtddrenlrly 25

-----
1 match found in sequence:
R83094 ; HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
  (from "A-Geneseq 26")
ID R83094 standard; peptide; 10 AA.
AC R83094;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.

```

```

PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 14; Page 34; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with
CC a subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA;
SQ 1 A; 3 R; 0 N; 1 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

1
1 redrillry
1 10
-----
1 match found in sequence:
R83096 : HLA-B*2702 CTL modulating peptide (B2702.75-84(L)).
(from "A-Geneseq 26")
ID R83096 standard; peptide; 10 AA.
AC R83096;
DE 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.75-84(L)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 14; Page 34; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with
CC a subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA;
SQ 0 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 3 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

1
1 renrillry
1 10
-----

```

```

1 match found in sequence:
R92907 : HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84).
(from "A-Geneseq 26")
ID R92907 standard; peptide; 20 AA.
AC R92907;
DE 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

1
1 yrlairlnerenrillry
1 20
-----
1 match found in sequence:
R92908 : HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84).
(from "A-Geneseq 26")
ID R92908 standard; peptide; 20 AA.
AC R92908;
DE 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime

```

CC administration for current treatments). The peptides particularly
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
 CC of the patient.
 SQ Sequence 20 AA;
 SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
 SQ 1 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 1 T; 0 W; 2 Y; 0 V;
 Found using 'seq1' (seq1.key)

1 yrlatlnrerrenlrialy 20
 11

 1 match found in sequence:
 R95413 : Alpha1-helix of HLA-B2702.
 (from "A-Geneseq 26")
 ID R95413 standard; peptide: 10 AA.
 AC R95413;
 DE 12-NOV-1996 (first entry)
 DT Alpha1-helix of HLA-B2702.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 11; 29pp; English.
 CC This sequence represents the alpha1-helix of the
 CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 10 AA;
 SQ 1 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
 SQ 1 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
 Found using 'seq1' (seq1.key)

1 renlrialy 10
 1

 1 match found in sequence:
 R95428 : HLA-B2702 84-75-84 palindrome.
 (from "A-Geneseq 26")
 ID R95428 standard; peptide: 20 AA.
 AC R95428;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75-84 palindrome.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;

KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
 CC compounds can be screened for their effect on the cytolytic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;
 SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
 SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
 Found using 'seq1' (seq1.key)

1 yrlatlnrerrenlrialy 20
 11

 1 match found in sequence:
 R95430 : HLA-B2702 84-75/75-84T palindrome.
 (from "A-Geneseq 26")
 ID R95430 standard; peptide: 20 AA.
 AC R95430;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702 84-75/75-84T palindrome.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; U12985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI: 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.
 PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B2702 84-75/75-84T palindrome. These sequences can be used to
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
 CC membrane protein associated with T-cell activation in mammalian T-cells,
 CC and is also immunologically cross reactive with the heat shock protein
 CC Hsc70. p74 is found in a limited number of cell types, but is

CC particularly expressed on B and T cells. p74 can be isolated by lysis of
 CC a suitable cell with an amphoteric detergent, and then passed through an
 CC affinity column containing a covalently bound HLA-B2702 palindromic
 CC peptide. Compositions comprising the extracellular fragment of p74
 CC combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.
 CC candidate compounds can be screened for their effect on the cytotoxic
 CC activity of T-cells, by combining them with the extracellular portion of
 CC p74 and determining the amount of binding between the candidate compound
 CC and p74. Modulation of CTL activity can be inhibited in a cellular
 CC composition containing T-cells and antigen presenting cells (APCs), by
 CC adding to the mix the extracellular portion of p74, in an amount
 CC sufficient to compete with p74 for the binding of the p74 ligand.
 SQ Sequence 20 AA;
 SQ 2 A; 5 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
 SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 2 T; 0 W; 1 Y; 0 V;
 Found using 'seq1' (seq1.key)

1 yrlairnretrenlrlr 20
 11
 |-----|

1 match found in sequence:

R95431 ; HLA-B7.60-84.
 (from "A-Geneseq 26")
 ID R95431 standard; peptide; 25 AA.
 AC R95431; 1996 (first entry)
 DT 12-NOV-1996
 DE HLA-B7.60-84.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.

PR 10-NOV-1994; UI2985.
 PR 10-NOV-1993; US-150493.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.
 PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 12; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC HLA-B7.60-84. These sequences can be used to isolate the protein p74
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein
 CC associated with T-cell activation in mammalian T-cells, and is also
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
 CC found in a limited number of cell types, but is particularly expressed on
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
 CC amphoteric detergent, and then passed through an affinity column
 CC containing a covalently bound HLA-B2702 palindromic peptide.

CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytotoxic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.

SQ Sequence 25 AA;
 SQ 2 A; 4 R; 1 N; 2 D; 0 B; 1 C; 2 Q; 2 E; 0 Z; 1 G; 0 H;
 SQ 1 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 1 Y; 0 V;
 Found using 'seq1' (seq1.key)

|-----|

6 gickakagtireslrlr 25
 16

1 match found in sequence:

R95415 ; HLA-B7.84-75-84 Palindrome.
 (from "A-Geneseq 26")
 ID R95415 standard; peptide; 20 AA.
 AC R95415;
 DT 12-NOV-1996 (first entry)
 DE HLA-B7.84-75-84 Palindrome.
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.

PR 10-NOV-1994; UI2985.
 PR 10-NOV-1993; US-150493.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Clayberger C, Krensky AM;
 DR WPI; 95-194027/25.

PT Compsns. comprising lymphoid surface membrane proteins - which may
 PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 18; 29pp; English.
 CC R95413, and R95415-R95431 represent palindromes and fragments of
 CC human-leucocyte-associated antigens. This sequence represents the
 CC HLA-B7.84-75/85-84 palindrome. These sequences can be used to isolate
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
 CC protein associated with T-cell activation in mammalian T-cells, and is
 CC also immunologically cross reactive with the heat shock protein Hsc70.
 CC p74 is found in a limited number of cell types, but is particularly
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
 CC cell with an amphoteric detergent, and then passed through an affinity
 CC column containing a covalently bound HLA-B2702 palindromic peptide.
 CC Compositions comprising the extracellular fragment of p74 combined with
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
 CC compounds can be screened for their effect on the cytotoxic activity of
 CC T-cells, by combining them with the extracellular portion of p74 and
 CC determining the amount of binding between the candidate compound and p74.
 CC Modulation of CTL activity can be inhibited in a cellular composition
 CC containing T-cells and antigen presenting cells (APCs), by adding to the
 CC mix the extracellular portion of p74, in an amount sufficient to compete
 CC with p74 for the binding of the p74 ligand.

SQ Sequence 20 AA;
 SQ 0 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 2 G; 0 H;
 SQ 0 I; 4 L; 0 K; 0 M; 0 F; 0 P; 2 S; 0 T; 0 W; 2 Y; 0 V;
 Found using 'seq1' (seq1.key)

1 ygrlnrlserreslrlr 20
 11
 |-----|

1 match found in sequence:

R95416 ; HLA-B2702.60-84.
 (from "A-Geneseq 26")
 ID R95416 standard; peptide; 25 AA.
 AC R95416;
 DT 12-NOV-1996 (first entry)
 DE HLA-B2702.60-84
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
 KW cytolysis; antigen presenting cell.
 OS Synthetic.
 PN WO9513288-A1.
 PD 18-MAY-1995.

PR 10-NOV-1994; UI2985.
 PR 10-NOV-1993; US-150493.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

```

PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents
CC HLA-B*2702.60-84. These sequences can be used to isolate the protein p74
CC from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC this sequence, induces calcium influx, and inhibits cytotoxic T
CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can
CC be screened for their effect on the cytolytic activity of T-cells, by
CC combining them with the extracellular portion of p74 and determining the
CC amount of binding between the candidate compound and p74. Modulation of
CC CTL activity can be inhibited in a cellular composition containing
CC T-cells and antigen presenting cells (APCs), by adding to the mix the
CC extracellular portion of p74, in an amount sufficient to compete with p74
CC for the binding of the p74 ligand.
SQ Sequence 25 AA;
SQ 3 A; 4 R; 1 N; 2 D; 0 B; 1 C; 2 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 2 K; 0 M; 0 F; 0 P; 0 S; 2 T; 1 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)
...
1 match found in sequence:
R95418 : HLA-B*46.60-84.
(from "A-Geneseq 26")
ID R95418 standard; peptide; 25 AA.
AC R95418;
DE HLA-B*46.60-84.
KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytotoxicity; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B*46.60-84. These sequences can be used to isolate the protein p74
CC from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
CC compounds can be screened for their effect on the cytolytic activity of

```

```

CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 25 AA;
SQ 1 A; 5 R; 1 N; 2 D; 0 B; 0 C; 3 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 2 Y; 1 V;
Found using 'seq1' (seq1.key)
...
1 match found in sequence:
R95419 : HLA-B*62.60-84.
(from "A-Geneseq 26")
ID R95419 standard; peptide; 25 AA.
AC R95419;
DE HLA-B*62.60-84.
KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytotoxicity; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B*62.60-84. These sequences can be used to isolate the protein p74
CC from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
CC compounds can be screened for their effect on the cytolytic activity of

```

```

R95422 ; HLAB38.6084.
ID (from "A-GenesSeq 26")
AC R95422; standard; peptide; 25 AA.
DT 12-NOV-1996 (first entry)
DE HLAB38.6084.
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PF 18-MAY-1995.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C. Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702.75-84(D). These sequences can be used to isolate the protein
CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 25 AA;
SQ 1 A; 4 R; 3 N; 1 D; 0 B; 1 C; 2 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)
...
6 qickntntqrenriialry 25
1-----|
16

```

```

PI Clayberger C. Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 11; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702.75-84(D). These sequences can be used to isolate the protein
CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 10 AA;
SQ 1 A; 3 R; 0 N; 1 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)
1-----|
1 redtrialry
1 10
-----
1 match found in sequence:
HLHUB7 ; MHC class I histocompatibility antigen HLA-B7 alpha chain
(from "PIR 50")
ENTRY HLHUB7 #type complete
TITLE MHC class I histocompatibility antigen HLA-B7 alpha chain
precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Jul-1980 #sequence_revision 22-Apr-1995 #text_change
06-Sep-1996
ACCESSIONS B35997; A90435; A93840; A02185
REFERENCE A35997
#authors Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2833-2837
#title Rapid cloning of HLA-A,B CDNA by using the polymerase chain
reaction: frequency and nature of errors produced in
amplification.
#cross-references MUID:90207291
#accession B35997
#molecule_type mRNA
#residues 1-362 #label ENN
#cross-references GB:M32317
#note this allele is designated B*0702 (previously HLA-B*7.2)
REFERENCE A90435
#authors Orr, H.T.; Lopez de Castro, J.A.; Lancet, D.; Strominger,
J.L.
#journal Biochemistry (1979) 18:5711-5720
#title Complete amino acid sequence of a papain-solubilized human
histocompatibility antigen, HLA-B7. 2. Sequence
determination and search for homologies.
#cross-references MUID:80088278
#accession A90435
#molecule_type protein
#residues 25-265, 'E', 267-295 #label ORR
REFERENCE A93840
#authors Tragardh, L.; Rask, L.; Wiman, K.; Fohlman, J.; Peterson,
P.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1980) 77:1129-1133
#title Complete amino acid sequence of pooled papain-solubilized

```

```

HLA-A, -B, and -C antigens: relatedness to immunoglobulins
and internal homologies.
#cross-references MUID:80145722
#accession A93840
##molecule_type protein
##residues 25-42,'Q','44-47','A','49-53','N','55-68','Q','70-86','Q','88-93,
'H','95-139','TRAI','141-175','A','177-198','R','200-246','N',
248-251,'N','253-297 #label TRA
##experimental_source pooled HLA-A, -B, and -C antigens
##note this sequence represents the predominant amino acid at
each position

GENETICS
#gene GDB:HLA-B
##cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-114 #domain alpha-1 #label EX1\
115-206 #domain alpha-2 #label EX2\
220-285 #domain immunoglobulin homology #label IMM\
307-331 #domain transmembrane #status predicted #label TMM\
332-362 #domain intracellular #status predicted #label INT\
110 #binding_site carbohydrate (Asn) (covalent) #status
experimental\
125-188,227-283 #disulfide_bonds #status experimental
SUMMARY #length 362 #molecular_weight 40460 #checksum 8234
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qiykaqatdreslnrlgynyngseagsh
99
108
|-----|
#type fragment
HLHU40 MHC class I histocompatibility antigen HLA-B40 alpha chain -
human (fragment)
#formal_name Homo sapiens #common_name man
28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
06-Sep-1996
ACCESSIONS A02186
REFERENCE Lopez de Castro, J.A.; Bragado, R.; Strong, D.M.; Strominger,
J.L.
#journal Biochemistry (1983) 22:3961-3969
#title Primary structure of papain-solubilized human
histocompatibility antigen HLA-B40 (-Bw60). An outline of
alloantigenic determinants.
#cross-references MUID:84000412
#accession A02186
##molecule_type protein
##residues 1-270 #label LOP
COMMENT Comparison of a number of class I allelic sequences (-B40 vs. -B7
and -A2 vs. -A28) indicates that the distribution of differences
among the respective alleles (polymorphism) is essentially
restricted to the alpha-1 and alpha-2 domains. The most
conspicuous clustering of variability between the -B40 and -B7
alleles occurs between residues 63-74. This segment and residues
147-156 are possible alloantigenic determinants of these
antigens.

GENETICS
#gene GDB:HLA-B

```

```

##cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; membrane protein;
transplantation antigen
FEATURE
1-90 #domain alpha-1 #label EX1\
91-181 #domain alpha-2 #label EX2\
135-260 #domain immunoglobulin homology #label IMM\
86 #binding_site carbohydrate (Asn) (covalent) #status
experimental\
101-163,202-258 #disulfide_bonds #status predicted
SUMMARY #length 270 #checksum 4804
SEQUENCE
Found using 'seq1' (seq1.key)
...
65 qiskntqttyreslnrlgynyngseagsh
75
84
|-----|
#type complete
HLHU12 MHC class I histocompatibility antigen HLA alpha chain
ENTRY precursor (clone pHLA 12.4) - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change
DATE 15-Jun-1996
ACCESSIONS A02189
REFERENCE Malissen, M.; Malissen, B.; Jordan, B.R.
#authors Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
#journal Exon/intron organization and complete nucleotide sequence of
#title an HLA gene.
#cross-references MUID:82151002
#accession A02189
##molecule_type DNA
##residues 1-359 #label MAL
COMMENT The seven exons correspond approximately to the domain structure of
this chain.
GENETICS
#map_position 6p21.3
#introns 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
FEATURE
1-21 #domain signal sequence #status predicted #label SIG\
22-359 #product class I histocompatibility antigen HLA alpha
chain #status predicted #label MAL\
22-304 #domain extracellular #status predicted #label EXT\
22-111 #domain alpha-1 #label EX1\
112-203 #domain alpha-2 #label EX2\
217-282 #domain immunoglobulin homology #label IMM\
305-329 #domain transmembrane #status predicted #label TMM\
335-359 #domain intracellular #status predicted #label INT\
107 #binding_site carbohydrate (Asn) (covalent) #status
predicted\
224-280 #disulfide_bonds #status predicted
SUMMARY #length 359 #molecular_weight 40548 #checksum 2195
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```

86      gckagaqterlnrlryngseggsh
      96
      |-----|
      105
      ...

-----
1 match found in sequence:
HLHUW3 ; MHC class I histocompatibility antigen HLA-Cw3 alpha chain
ENTRY (from "PIR 50")
TITLE HLHUW3 #type complete
MHC class I histocompatibility antigen HLA-Cw3 alpha chain
precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
06-Sep-1996
ACCESSIONS A02190
REFERENCE A02190
#authors Sodoyer, R.; Damotte, M.; Delovitch, T.L.; Trucy, J.; Jordan,
B.R.; Strachan, T.
#journal EMBO J. (1984) 3:879-885
#title Complete nucleotide sequence of a gene encoding a functional
human class I histocompatibility antigen (HLA-CW3).
#cross-references MUID:84207947
#accession A02190
#molecule_type DNA
#residues 1-366 #label SOD
GENETICS
#gene GDB:HLA-C
#cross-references GDB:119311
#map_position 6p21.3-6p21.3
#introns 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
#keywords duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-366 #product class I histocompatibility antigen HLA-Cw3\
alpha chain #status predicted #label MAT\
25-307 #domain extracellular #status predicted #label EXT\
25-114 #domain alpha-1 #label EX1\
115-206 #domain alpha-2 #label EX2\
220-285 #domain immunoglobulin homology #label IMM\
308-332 #domain transmembrane #status predicted #label TM\
333-366 #domain intracellular #status predicted #label INT\
110 #binding_site carbohydrate (Asn) (covalent) #status
predicted\
227-283 #disulfide_bonds #status predicted
SUMMARY #length 366 #molecular-weight 40744 #checksum 4249
SEQUENCE
Found using 'seq1' (seq1.key)
...

89      qxykpaqtdrvslrnlryngseagshi
      99
      |-----|
      108
      ...

-----
1 match found in sequence:
HLHUC4 ; MHC class I histocompatibility antigen HLA-C4 alpha chain -
ENTRY (from "PIR 50")
TITLE HLHUC4 #type complete
MHC class I histocompatibility antigen HLA-C4 alpha chain -
human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
06-Sep-1996
ACCESSIONS A24512
REFERENCE A92500

```

```

#authors Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
#journal J. Biol. Chem. (1985) 260:13414-13423
#title Comparison of HLA class I gene sequences. Derivation of
locus-specific oligonucleotide probes specific for HLA-A,
HLA-B, and HLA-C genes.
#cross-references MUID:86033791
#accession A24512
#molecule_type DNA
#residues 1-342 #label DAV
GENETICS
#gene GDB:HLA-C
#cross-references GDB:119311
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
#keywords glycoprotein; heterodimer; transmembrane protein;
transplantation antigen
FEATURE
196-261 #domain immunoglobulin homology #label IMM
SUMMARY #length 342 #molecular-weight 38082 #checksum 7418
SEQUENCE
Found using 'seq1' (seq1.key)
...

65      qkykqaqadrvslrnlryngsqsgsht
      75
      |-----|
      84
      ...

-----
1 match found in sequence:
HLHU32 ; MHC class I histocompatibility antigen HLA-A32 alpha chain -
ENTRY (from "PIR 50")
TITLE HLHU32 #type fragment
MHC class I histocompatibility antigen HLA-A32 alpha chain -
human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
06-Sep-1996
ACCESSIONS A26088
REFERENCE A26088
#authors Wan, A.M.; Ennis, P.; Parham, P.; Holmes, N.
#journal J. Immunol. (1986) 137:3671-3674
#title The primary structure of HLA-A32 suggests a region involved
in formation of the Bw4/Bw6 epitopes.
#cross-references MUID:87058961
#accession A26088
#molecule_type protein
#residues 1-274 #label WAN
GENETICS
#gene GDB:HLA-A
#cross-references GDB:119310
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
#keywords glycoprotein; heterodimer; transmembrane protein;
transplantation antigen
FEATURE
196-261 #domain immunoglobulin homology #label IMM
SUMMARY #length 274 #checksum 899
SEQUENCE
Found using 'seq1' (seq1.key)
...

65      rnvkhsqtdreslrlryngsqsgsht
      75
      |-----|
      84
      ...

```

```

-----
1 match found in sequence:
HLHUB8 : MHC class I histocompatibility antigen HLA-B*58 alpha chain
      (from "PIR 50")
ENTRY   HLHUB8      #type complete
TITLE   MHC class I histocompatibility antigen HLA-B*58 alpha chain
      precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
      06-Sep-1996
ACCESSIONS A23895
REFERENCE   A23895
#authors   Ways, J.P.; Coppin, H.L.; Parham, P.
#journal   J. Biol. Chem. (1985) 260:11924-11933
#title     The complete primary structure of HLA-B*58.
#cross-references MUID:86008247
#accession A23895
#molecule_type DNA
#residues  1-362 #label WAY
#note      the authors translated the codon GCC for residue 349 as
      Ser
COMMENT    This protein is a subtype of the HLA-B17 family.
GENETICS
#gene      GDB:HLA-B
#cross-references GDB:120048
#map_position 6p21.3-6p21.3
#introns   25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
      immunoglobulin homology
KEYWORDS     duplication; glycoprotein; heterodimer; transmembrane
      protein; transplantation antigen
FEATURE
1-24      #domain signal sequence #status predicted #label SIG\
25-362    #product class I histocompatibility antigen HLA-B*58
      alpha chain #status predicted #label MAY\
25-307    #domain extracellular #status predicted #label EXT\
25-114    #domain alpha-1 #label EX1\
115-206   #domain alpha-2 #label EX2\
220-285   #domain immunoglobulin homology #label IMM\
308-331   #domain transmembrane #status predicted #label TMM\
332-362   #domain intracellular #status predicted #label INT\
SUMMARY
SEQUENCE   #length 362 #molecular_weight 40321 #checksum 8057
Found using 'seq1' (seq1.key)
...
89  rmkasaqtyrenlrialryngseagshi
      |-----|
      99      108
...
-----
1 match found in sequence:
HLMSDB : MHC class I histocompatibility antigen H-2D(b) alpha chain -
      (from "PIR 50")
ENTRY   HLMSDB      #type complete
TITLE   MHC class I histocompatibility antigen H-2D(b) alpha chain -
      mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     29-Jul-1981 #sequence_revision 14-Nov-1983 #text_change
      04-Dec-1994
ACCESSIONS A91747; A92315; A91748; A02200
REFERENCE   A91747
#authors   Reyes, A.A.; Schold, M.; Wallace, R.B.
#journal   Immunogenetics (1982) 16:1-9
#title     The complete amino acid sequence of the murine
      transplantation antigen H-2D(b) as deduced by molecular
      cloning
#cross-references MUID:83005712
#accession A91747
#molecule_type mRNA

```

```

#residues 1-338 #label REY
REFERENCE A92315
#authors  Maloy, W.L.; Nathenson, S.G.; Coligan, J.E.
#journal  J. Biol. Chem. (1981) 256:2863-2872
#title    Primary structure of murine major histocompatibility complex
      alloantigens. Amino acid sequence of the NH-2-terminal
      ninety-eight residues of the H-2D(b) glycoprotein.
#cross-references MUID:81142266
#accession A92315
#molecule_type protein
#residues 1-98 #label MAI
REFERENCE A91748
#authors  Maloy, W.L.; Coligan, J.E.
#journal  Immunogenetics (1982) 16:11-22
#title    Primary structure of the H-2D(b) alloantigen. II. Additional
      amino acid sequence information, localization of a third
      site of glycosylation and evidence for K and D region
      specific sequences.
#cross-references MUID:83005713
#accession A91748
#molecule_type protein
#residues 229-284; 308-332, 'X', 334 #label MA2
GENETICS
#introns  91/1; 183/1; 275/1; 314/1; 325/1; 338/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
      immunoglobulin homology
KEYWORDS     duplication; glycoprotein; heterodimer; transmembrane protein
FEATURE
1-283      #domain extracellular #status predicted #label EXT\
1-90       #domain alpha-1 #label EX1\
91-182     #domain alpha-2 #label EX2\
196-261    #domain immunoglobulin homology #label IMM\
284-307    #domain transmembrane #status predicted #label TMM\
314-338    #domain intracellular #status predicted #label INT\
86,256     #binding_site carbohydrate (Asn) (covalent) #status
      experimental\
101-164,203-259 #disulfide_bonds #status predicted\
176         #binding_site carbohydrate (Asn) (covalent) #status
      predicted
SUMMARY      #length 338 #molecular_weight 38402 #checksum 4501
SEQUENCE
Found using 'seq1' (seq1.key)
...
65  qkagqeqwfrvslrnllyngsaggsht
      |-----|
      75      84
...
-----
1 match found in sequence:
A30547 : class I histocompatibility antigen H-2D-b alpha chain - mouse
      (from "PIR 50")
ENTRY   A30547      #type fragment
TITLE   class I histocompatibility antigen H-2D-b alpha chain - mouse
      (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
      12-Apr-1995
ACCESSIONS A30547
REFERENCE   A30547
#authors   Duran, L.W.; Horton, R.M.; Birschbach, C.W.; Chang-Miller,
      A.; Pease, L.R.
#journal   J. Immunol. (1989) 142:288-296
#title     Structural relationships among the H-2 D-regions of murine
      MHC haplotypes.
#accession A30547
#molecule_type DNA
#residues 1-206 #label DUR
CLASSIFICATION #superfamily class I histocompatibility antigen;
      immunoglobulin homology

```

```
SUMMARY          #length 206 #checksum 9521
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qkagqeqwfrvslrnllyngysaggsht
    |-----|
    99 108
...
-----
1 match found in sequence:
A49411 : human leukocyte antigen, HLA-C (alpha 1 and 2 domains) -
(from "PIR 50")
ENTRY   A49411      #type fragment
TITLE   human leukocyte antigen, HLA-C (alpha 1 and 2 domains) -
        human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
        02-Jun-1995
ACCESSIONS A49411
REFERENCE  A49411
#authors   Falk, K.; Rotzschke, O.; Grahovac, B.; Schendel, D.;
           Stevanovic, S.; Gnau, V.; Jung, G.; Strominger, J.L.;
           Rammensee, H.G.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1993) 90:12005-12009
#title     Allele-specific peptide ligand motifs of HLA-C molecules.
#cross-references MUID:94089758
#accession A49411
#status    preliminary
#molecule_type protein
#residues  1-182 #label FAL
#cross-references NCBI:P141047
#experimental_source Ctr cell line
#note      sequence extracted from NCBI backbone
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
SUMMARY          #length 182 #checksum 3873
SEQUENCE
Found using 'seq1' (seq1.key)
...
65  qkyrqaqadrvslrnllyngysaggsht
    |-----|
    75 84
...
-----
1 match found in sequence:
A35997 : MHC class I histocompatibility antigen HLA-A25 alpha chain
(from "PIR 50")
ENTRY   A35997      #type complete
TITLE   MHC class I histocompatibility antigen HLA-A25 alpha chain
        precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change
        26-Apr-1996
ACCESSIONS A35997
REFERENCE  A35997
#authors   Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2833-2837
#title     Rapid cloning of HLA-A,B cDNA by using the polymerase chain
           reaction: frequency and nature of errors produced in
           amplification.
#cross-references MUID:90207291
#accession A35997
#status    preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues  1-364 #label ENN

##cross-references GB:M32321
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE       219-284      #domain immunoglobulin homology #label IMM
SUMMARY          #length 364 #molecular-weight 41147 #checksum 1931
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  rnvhahsqtdreslrnllyngysaggsht
    |-----|
    99 108
...
-----
1 match found in sequence:
S03537 : class I histocompatibility antigen ChLA-B1 alpha chain
(from "PIR 50")
ENTRY   S03537      #type complete
TITLE   class I histocompatibility antigen ChLA-B1 alpha chain
        precursor - chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE     18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change
        26-Apr-1996
ACCESSIONS S03537
REFERENCE  S01171
#authors   Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer,
           G.; Klein, J.
#journal   EMBO J. (1988) 7:2765-2774
#title     Nucleotide sequences of chimpanzee MHC class I alleles:
           evidence for trans-species mode of evolution.
#cross-references MUID:89030641
#accession S03537
#molecule_type mRNA
#residues  1-363 #label MAY
#cross-references EMBL:X13115
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
KEYWORDS    transmembrane protein
FEATURE     1-24
           25-363      #domain signal sequence #label SIG\
           #product class I histocompatibility antigen alpha chain
           #label MAY\
           #domain extracellular #label EXT\
           #domain immunoglobulin homology #label IMM\
           #domain transmembrane #label TMM\
           #domain intracellular #label INT
SUMMARY          #length 363 #molecular-weight 40633 #checksum 1865
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  rnmkasatdrenlrnllyngysaggsht
    |-----|
    99 108
...
-----
1 match found in sequence:
S03538 : class I histocompatibility antigen ChLA-B2 alpha chain
(from "PIR 50")
ENTRY   S03538      #type fragment
TITLE   class I histocompatibility antigen ChLA-B2 alpha chain
        precursor - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE     18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change
        26-Apr-1996
ACCESSIONS S03538
```

```

REFERENCE      S01171
#authors      Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer,
               G.; Klein, J.
#journal      EMBO J. (1988) 7:2765-2774
#title        Nucleotide sequences of chimpanzee MHC class I alleles:
               evidence for trans-species mode of evolution.
#cross-references MUID:89030641
#accession    S03538
#molecule_type mRNA
##residues    1-358 #label MAY
##cross-references EMBL:X13116
##note        the four residues preceding 1-Ala shown in Fig. 6 were
               apparently misplaced from the sequence of the CHIA-B1
               protein
#note        the authors translated the codon CCG for residue 125 as
               Ser
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
KEYWORDS       transmembrane protein
FEATURE        1-20
               #domain signal sequence (fragment) #label SIG\
               #product class I histocompatibility antigen alpha chain
               #label MAY\
               #domain extracellular #label EXT\
               #domain immunoglobulin homology #label IMM\
               #domain transmembrane #label TM\
               #domain intracellular #label INT
               #length 358 #checksum 1496
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
85  qisktnaqtqyreslnrlryynqseagshi
    |-----|
    95
    104
...
1 match found in sequence:
B30345 ; MHC class I histocompatibility antigen HLA-Bw52 precursor -
(from "PIR 50")
ENTRY
TITLE      MHC class I histocompatibility antigen HLA-Bw52 precursor -
           human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
           26-Apr-1996
ACCESSIONS  B30345
REFERENCE    A30345
#authors     Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
           P.; Kano, K.; Takiguchi, M.
#journal     J. Immunol. (1989) 142:306-311
#title       HLA-B51 and HLA-Bw52 differ by only two amino acids which are
           in the helical region of the alpha-1 domain.
#cross-references MUID:89080265
#accession   B30345
#status      preliminary
#molecule_type DNA
##residues   1-362 #label HAY
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE      220-285
               #domain immunoglobulin homology #label IMM
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qisktnqtqyrenrlrlryynqseagsh
    |-----|
    95
    108

```

```

99 108
...
1 match found in sequence:
JH0541 ; Class I histocompatibility antigen Gogo-B0103 heavy chain
(from "PIR 50")
ENTRY
TITLE      JH0541 #type complete
           class I histocompatibility antigen Gogo-B0103 heavy chain
           precursor - lowland gorilla
ORGANISM    #formal_name Gorilla gorilla #common_name lowland
           gorilla
DATE        30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
           26-Apr-1996
ACCESSIONS  JH0541
REFERENCE    JH0534
#authors     Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
#journal     J. Exp. Med. (1991) 174:1491-1509
#title       Gorilla class I major histocompatibility complex alleles:
           comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession   JH0541
#molecule_type DNA
##residues   1-362 #label LAW
##cross-references EMBL:X60254
##experimental_source EBV-transformed B cell
GENETICS
#introns     25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE      1-24
               #domain signal sequence #label SIG\
               #product class I histocompatibility antigen heavy chain,
               Gogo-B0103 #status predicted #label CLA\
               #domain alpha-1 #label AL1\
               #domain alpha-2 #label AL2\
               #domain alpha-3 #label AL3\
               #domain immunoglobulin homology #label IMM\
               #domain intracellular #label INT
               #length 362 #molecular-weight 40248 #checksum 7416
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qtskaqadtrenrlrlryynqseagsh
    |-----|
    99
    108
...
1 match found in sequence:
JH0539 ; Class I histocompatibility antigen Gogo-B0101 heavy chain
(from "PIR 50")
ENTRY
TITLE      JH0539 #type complete
           class I histocompatibility antigen Gogo-B0101 heavy chain
           precursor - lowland gorilla
ORGANISM    #formal_name Gorilla gorilla #common_name lowland
           gorilla
DATE        30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
           26-Apr-1996
ACCESSIONS  JH0539
REFERENCE    JH0534
#authors     Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
#journal     J. Exp. Med. (1991) 174:1491-1509
#title       Gorilla class I major histocompatibility complex alleles:
           comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession   JH0539
#molecule_type DNA
##residues   1-362 #label LAW

```

```

####cross-references EMBL:X60255
GENETICS   ##experimental_source EBV-transformed B cell
#introns   25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE
1-24        #domain signal sequence #label SIG\
25-362      #product class I histocompatibility antigen heavy chain,
               Gogo-B0101 #status predicted #label CLA\
25-114      #domain alpha-1 #label AL1\
115-206     #domain alpha-2 #label AL2\
207-298     #domain alpha-3 #label AL3\
220-285     #domain immunoglobulin homology #label IMM\
299-362     #domain intracellular #label INT
SUMMARY     #length 362 #molecular-weight 40170 #checksum 7327
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qtskaqaqtdrenlrirlyynqseagsh
    |-----|
    99 108

####cross-references EMBL:X60255
GENETICS   ##experimental_source EBV-transformed B cell
#introns   25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE
1-24        #domain signal sequence #label SIG\
25-362      #product class I histocompatibility antigen heavy chain,
               Gogo-B0102 #status predicted #label CLA\
25-114      #domain alpha-1 #label AL1\
115-206     #domain alpha-2 #label AL2\
207-298     #domain alpha-3 #label AL3\
220-285     #domain immunoglobulin homology #label IMM\
299-362     #domain intracellular #label INT
SUMMARY     #length 362 #molecular-weight 40204 #checksum 7312
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qtskaqaqtdrenlrirlyynqseagsh
    |-----|
    99 108

```

```

...
-----
1 match found in sequence:
S49381 ; class I major histocompatibility complex HLA-C alpha chain -
(from "PIR 50")
ENTRY      S49381 #type complete
TITLE      class I major histocompatibility complex HLA-C alpha chain -
             human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       16-Feb-1995 #sequence_revision 12-May-1995 #text_change
ACCESSIONS S49381
REFERENCE   S49381
#authors   Pablo, R.
#submission submitted to the EMBL Data Library, October 1994
#accession S49381
#status    preliminary
#molecule_type mRNA
#residues  1-366 #label PAB
#cross-references EMBL:X82122
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE     220-285 #domain immunoglobulin homology #label IMM
SUMMARY     #length 366 #molecular-weight 40915 #checksum 4194
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qkykrqaqadrvslrnlrgyngseagsh
    |-----|
    99 108

...
-----
1 match found in sequence:
S16789 ; class I histocompatibility antigen HLA-Bw72 alpha chain -
(from "PIR 50")
ENTRY      S16789 #type complete
TITLE      class I histocompatibility antigen HLA-Bw72 alpha chain -
             human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
ACCESSIONS S16789
REFERENCE   S16766
#authors   Madrigal, J.A.; Bellich, M.P.; Hildebrand, W.H.; Benjamin,
             R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
             Petzi-Erler, M.L.; Martell, R.W.; Du Toit, E.D.; Parham, P.
#submission submitted to the EMBL Data Library, August 1991
#description Molecular definition of HLA-A,B antigens of black
             populations: Implications for HLA matching and typing in
             transplantation.
#accession S16789
#molecule_type mRNA
#residues  1-362 #label MAD
#cross-references EMBL:X61709
GENETICS   #gene GDB:HLA-B
             #cross-references GDB:120048
             #map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE     220-285 #domain immunoglobulin homology #label IMM
SUMMARY     #length 362 #molecular-weight 40387 #checksum 408
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```

89      qiskntqtyreslnlrgyynqseagsh
      99
      108
      1-----1
      1 match found in sequence:
      A45880 ; MHC class I histocompatibility antigen HLA-B35 alpha chain
      ENTRY
      TITLE
      MHC class I histocompatibility antigen HLA-B35 precursor (clone
      10) - human
      #formal_name Homo sapiens #common_name man
      14-Feb-1992 #sequence_revision 03-Jun-1993 #text_change
      06-Sep-1996
      ACCESSIONS
      REFERENCE
      #authors
      Ooba T.; Hayashi, H.; Karaki, S.; Tanabe, M.; Kano, K.;
      Takiguchi, M.
      #journal
      Immunogenetics (1989) 30:76-80
      #title
      The structure of HLA-B35 suggests that it is derived from
      HLA-B*58 by two genetic mechanisms.
      #accession
      A45880
      #molecule_type DNA
      #residues
      1-362 #label OOB
      #cross-references GB:M28110; GB:M28111; GB:M28112;
      GB:M28113; GB:M28114; GB:M28115
      #note
      this allele is designated B*3501

...

89      qskntqtyreslnlrgyynqseagsh
      99
      108
      1-----1
      1 match found in sequence:
      D35997 ; MHC class I histocompatibility antigen HLA-B57 alpha chain
      ENTRY
      TITLE
      MHC class I histocompatibility antigen HLA-B57 alpha chain
      precursor - human
      ALTERNATE_NAMES
      HLA-B*57
      ORGANISM
      Homo sapiens #common_name man
      16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change
      06-Sep-1996
      ACCESSIONS
      REFERENCE
      #authors
      Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
      #journal
      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2833-2837
      #title
      Rapid cloning of HLA-A,B cDNA by using the polymerase chain
      reaction: frequency and nature of errors produced in
      amplification.
      #cross-references MUID:90207291
      #accession
      D35997
      #molecule_type mRNA
      #residues
      1-364 #label ENN
      #cross-references GB:M32318
      #note
      this allele is designated B*5701
      REFERENCE
      S12622
      #authors
      Isamat, M.; Girdlestone, J.; Milstein, C.
      #journal
      Nucleic Acids Res. (1990) 18:6702
      #title
      Nucleotide sequence of an HLA-B*57 gene.
      #cross-references MUID:91067476
      #accession
      S12622
      #molecule_type DNA
      #residues
      1-362 #label ISA
      #cross-references EMBL:X55711
      #note
      this allele is designated B*5701
      REFERENCE
      S16766
      #authors
      Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,

...

89      qifkntqtyreslnlrgyynqseagsh
      99
      108
      1-----1
      1 match found in sequence:
      D35997 ; MHC class I histocompatibility antigen HLA-B57 alpha chain
      ENTRY
      TITLE
      MHC class I histocompatibility antigen HLA-B57 alpha chain
      precursor - human
      ALTERNATE_NAMES
      HLA-B*57
      ORGANISM
      Homo sapiens #common_name man
      16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change
      06-Sep-1996
      ACCESSIONS
      REFERENCE
      #authors
      Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
      #journal
      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2833-2837
      #title
      Rapid cloning of HLA-A,B cDNA by using the polymerase chain
      reaction: frequency and nature of errors produced in
      amplification.
      #cross-references MUID:90207291
      #accession
      D35997
      #molecule_type mRNA
      #residues
      1-364 #label ENN
      #cross-references GB:M32318
      #note
      this allele is designated B*5701
      REFERENCE
      S12622
      #authors
      Isamat, M.; Girdlestone, J.; Milstein, C.
      #journal
      Nucleic Acids Res. (1990) 18:6702
      #title
      Nucleotide sequence of an HLA-B*57 gene.
      #cross-references MUID:91067476
      #accession
      S12622
      #molecule_type DNA
      #residues
      1-362 #label ISA
      #cross-references EMBL:X55711
      #note
      this allele is designated B*5701
      REFERENCE
      S16766
      #authors
      Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,

```

```

R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
Petzi-Erler, M.L.; Martelli, R.W.; Du Toit, E.D.; Parham, P.
submitted to the EMBL Data Library, August 1991
#description Molecular definition of HLA-A,B antigens of black
populations: Implications for HLA matching and typing in
transplantation.
#accession S16774
##molecule_type mRNA
##residues 1-137,'N',139,'Y',141-179,'R',181-362 ##label MAD
##cross-references EMBL:X61707
##note this allele is designated B*5702 (formerly Bw57.2)
GENETICS
#gene GDB:HLA-B
##cross-references GDB:120048
#map_position 6p21.3-6p21.3
#introns 25/2; 115/1; 207/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
220-285 #domain immunoglobulin homology #label IMM
SUMMARY #length 364 #molecular-weight 40451 #checksum 386
SEQUENCE
Found using 'seq1' (seq1.key)
...

1 match found in sequence:
A45834 ; MHC class I histocompatibility antigen HLA-B53 alpha chain
(from "PIR 50")
ENTRY
TITLE MHC class I histocompatibility antigen HLA-B53 alpha chain
precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change
06-Sep-1996
ACCESSIONS A45834
REFERENCE A45834
#authors Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.;
Takiguchi, M.
#journal Immunogenetics (1990) 32:195-199
#title Allospecificities between HLA-B*53 and HLA-B*35 are generated
by substitution of the residues associated with HLA-B*4/B*6
public epitopes.
#accession A45834
##molecule_type DNA
##residues 1-362 ##label HAV
##cross-references GB:M58636; GB:M33574
##note this allele is designated B*5301
GENETICS
#gene GDB:HLA-B
##cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
heterodimer; transmembrane protein
KEYWORDS
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
220-285 #domain immunoglobulin homology #label IMM\
110 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 362 #molecular-weight 40495 #checksum 9558
SEQUENCE
Found using 'seq1' (seq1.key)

```

```

...
89 qifkntqttyrenlriralyngseagsh
99
108

```

```

...
1 match found in sequence:
S24433 ; Class I histocompatibility antigen - human
(from "PIR 50")
ENTRY
TITLE S24433 #type complete
class I histocompatibility antigen - human
#formal_name Homo sapiens #common_name man
#cross-references EMBL:X61707
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24433
REFERENCE S24433
#authors Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal Nature (1992) 357:329-333
#title New recombinant HLA-B alleles in a tribe of South American
Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession S24433
##status preliminary
##molecule_type mRNA
##residues 1-354 ##label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
212-277 #domain immunoglobulin homology #label IMM
SUMMARY #length 354 #molecular-weight 39493 #checksum 5322
SEQUENCE
Found using 'seq1' (seq1.key)

```

```

...
81 qiskntqttyreslrnlrlyngseagsh
91
100

```

```

...
1 match found in sequence:
S24440 ; Class I histocompatibility antigen - human
(from "PIR 50")
ENTRY
TITLE S24440 #type complete
class I histocompatibility antigen - human
#formal_name Homo sapiens #common_name man
#cross-references EMBL:X61707
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24440
REFERENCE S24440
#authors Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal Nature (1992) 357:329-333
#title New recombinant HLA-B alleles in a tribe of South American
Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession S24440
##status preliminary
##molecule_type mRNA
##residues 1-354 ##label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
212-277 #domain immunoglobulin homology #label IMM
SUMMARY #length 354 #molecular-weight 39299 #checksum 5584
SEQUENCE

```

Found using 'seq1' (seq1.key)

```
...
81  qisktntqtdreslnlrgyngseagsht
    |-----|
    91 100
...

```

1 match found in sequence:

```
S24027 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      S24027      #type complete
TITLE      class I histocompatibility antigen - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24027
REFERENCE   S24027
#authors    Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
            E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
            Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal     Nature (1992) 357:329-333
#title       New recombinant HLA-B alleles in a tribe of South American
            Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession   S24027
#status      preliminary
#molecule_type mRNA
#residues    1-339 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
216-281      #domain immunoglobulin homology #label IMM
SUMMARY      #length 339 #molecular-weight 38073 #checksum 7431
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```
85  qisktntqtdreslnlrgyngseagsht
    |-----|
    95 104
...

```

1 match found in sequence:

```
S24437 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      S24437      #type complete
TITLE      class I histocompatibility antigen - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24437
REFERENCE   S24027
#authors    Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
            E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
            Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal     Nature (1992) 357:329-333
#title       New recombinant HLA-B alleles in a tribe of South American
            Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession   S24437
#status      preliminary
#molecule_type mRNA
#residues    1-354 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
212-277      #domain immunoglobulin homology #label IMM
SUMMARY      #length 354 #molecular-weight 39395 #checksum 6619
SEQUENCE

```

SEQUENCE
Found using 'seq1' (seq1.key)

```
...
81  qisktntqtdreslnlrgyngseagsht
    |-----|
    91 100
...

```

1 match found in sequence:

```
S24438 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      S24438      #type complete
TITLE      class I histocompatibility antigen - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24438
REFERENCE   S24027
#authors    Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
            E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
            Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal     Nature (1992) 357:329-333
#title       New recombinant HLA-B alleles in a tribe of South American
            Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession   S24438
#status      preliminary
#molecule_type mRNA
#residues    1-354 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
212-277      #domain immunoglobulin homology #label IMM
SUMMARY      #length 354 #molecular-weight 39403 #checksum 5245
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```
81  qisktntqtdreslnlrgyngseagsht
    |-----|
    91 100
...

```

1 match found in sequence:

```
S24434 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      S24434      #type complete
TITLE      class I histocompatibility antigen - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24434
REFERENCE   S24027
#authors    Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
            E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
            Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal     Nature (1992) 357:329-333
#title       New recombinant HLA-B alleles in a tribe of South American
            Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession   S24434
#status      preliminary
#molecule_type mRNA
#residues    1-362 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
220-285      #domain immunoglobulin homology #label IMM
SEQUENCE

```

SUMMARY #length 362 #molecular-weight 40462 #checksum 9855
 SEQUENCE
 Found using 'seq1' (seq1.key)
 ...

89 qifkntqtyrenlrlryynqseagshi
 99 108
 ...

 1 match found in sequence:
 S24436 : class I histocompatibility antigen - human
 (from "PIR 50")
 ENTRY S24436 #type complete
 TITLE class I histocompatibility antigen - human
 #formal_name Homo sapiens #common_name man
 ORGANISM
 DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
 26-Apr-1996
 S24436
 S24027
 #authors
 Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
 E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
 Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
 #journal
 Nature (1992) 357:329-333
 #title
 New recombinant HLA-B alleles in a tribe of South American
 Amerindians indicate rapid evolution of MHC class I loci.
 #cross-references MUID:92269956
 #accession S24436
 #status preliminary
 #molecule_type mRNA
 #residues 1-354 #label WAT
 CLASSIFICATION #superfamily immunoglobulin homology
 FEATURE
 212-277
 #domain immunoglobulin homology #label IMM
 SUMMARY #length 354 #molecular-weight 39558 #checksum 5505
 SEQUENCE
 Found using 'seq1' (seq1.key)
 ...

81 qifkntqtyrenlrlryynqseagshi
 91 100
 ...

 1 match found in sequence:
 S24435 : class I histocompatibility antigen - human
 (from "PIR 50")
 ENTRY S24435 #type complete
 TITLE class I histocompatibility antigen - human
 #formal_name Homo sapiens #common_name man
 ORGANISM
 DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
 26-Apr-1996
 S24435
 S24027
 #authors
 Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
 E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
 Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
 #journal
 Nature (1992) 357:329-333
 #title
 New recombinant HLA-B alleles in a tribe of South American
 Amerindians indicate rapid evolution of MHC class I loci.
 #cross-references MUID:92269956
 #accession S24435
 #status preliminary
 #molecule_type mRNA
 #residues 1-362 #label WAT
 CLASSIFICATION #superfamily immunoglobulin homology
 FEATURE

220-285 #domain immunoglobulin homology #label IMM
 SUMMARY #length 362 #molecular-weight 40396 #checksum 249
 SEQUENCE
 Found using 'seq1' (seq1.key)
 ...

89 qifkntqtyrenlrlryynqseagshi
 99 108
 ...

 1 match found in sequence:
 S24439 : class I histocompatibility antigen - human
 (from "PIR 50")
 ENTRY S24439 #type complete
 TITLE class I histocompatibility antigen - human
 #formal_name Homo sapiens #common_name man
 ORGANISM
 DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
 26-Apr-1996
 S24439
 S24027
 #authors
 Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
 E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
 Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
 #journal
 Nature (1992) 357:329-333
 #title
 New recombinant HLA-B alleles in a tribe of South American
 Amerindians indicate rapid evolution of MHC class I loci.
 #cross-references MUID:92269956
 #accession S24439
 #status preliminary
 #molecule_type mRNA
 #residues 1-274 #label WAT
 CLASSIFICATION #superfamily immunoglobulin homology
 FEATURE
 196-261
 #domain immunoglobulin homology #label IMM
 SUMMARY #length 274 #molecular-weight 31614 #checksum 836
 SEQUENCE
 Found using 'seq1' (seq1.key)
 ...

65 qifkntqtdreslrlryynqseagst
 75 84
 ...

 1 match found in sequence:
 I37519 : MHC class I histocompatibility antigen HLA-B45 alpha chain
 (from "PIR 50")
 ENTRY I37519 #type complete
 TITLE MHC class I histocompatibility antigen HLA-B45 alpha chain
 precursor - human
 #formal_name Homo sapiens #common_name man
 ORGANISM
 DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
 06-Sep-1996
 I37519; S16772
 I37476
 #authors
 Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,
 R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
 Petzl-Erler, M.L.; Du Toit, E.D.; Parham, P.
 #journal
 J. Immunol. (1992) 149:3411-3415
 #title
 Distinctive HLA-A,B antigens of black populations formed by
 interallelic conversion.
 #cross-references MUID:93056508
 #accession I37519
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-362 #label RES

```

##cross-references EMBL:X61710; NID:g32182; CDS_PID:g32183
##note
this allele is designated B*4501
GENETICS
#gene
GDB:HLA-B
#map_position 6p21.3-6p21.3
#cross-references GDB:120048
CLASSIFICATION
#superfamily class I histocompatibility antigen;
immunoglobulin homology
heterodimer; transmembrane protein
KEYWORDS
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
220-285 #domain immunoglobulin homology #label IMM\
110 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY
#length 362 #molecular-weight 40414 #checksum 56
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qiskntqttyreslnrlgynyqseagsh
99
108
...
1 match found in sequence:
I37520 ; MHC class I histocompatibility antigen HLA-Bw50 alpha chain
(from "PIR 50")
ENTRY
TITLE
MHC class I histocompatibility antigen HLA-Bw50 alpha chain
ORGANISM
#formal_name Homo sapiens #common_name man
#precursor - human
DATE
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
I37520; S16773
REFERENCE
I37476
#authors
Madrigal, J.A.; Bellich, M.P.; Hildebrand, W.H.; Benjamin,
R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
Petzl-Erler, M.L.; Du Toit, E.D.; Parham, P.
J. Immunol. (1992) 149:3411-3415
#journal
#title
Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.
#cross-references MUID:93056508
#accession
I37520
#status
preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
##cross-references EMBL:X61706; NID:g32184; CDS_PID:g32185
GENETICS
#gene
GDB:HLA-B
#map_position 6p21.3-6p21.3
#cross-references GDB:120048
CLASSIFICATION
#superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SUMMARY
#length 362 #molecular-weight 40541 #checksum 123
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qiskntqttyreslnrlgynyqseagsh
99
108
...
1 match found in sequence:
I37522 ; MHC class I histocompatibility antigen HLA-Bw78 alpha chain
(from "PIR 50")
ENTRY
TITLE
MHC class I histocompatibility antigen HLA-Bw78 alpha chain
ORGANISM
#formal_name Homo sapiens #common_name man
#precursor - human
DATE
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
I37522; S16775
REFERENCE
I37476
#authors
Madrigal, J.A.; Bellich, M.P.; Hildebrand, W.H.; Benjamin,
R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
Petzl-Erler, M.L.; Du Toit, E.D.; Parham, P.
J. Immunol. (1992) 149:3411-3415
#journal
#title
Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.
#cross-references MUID:93056508
#accession
I37522
#status
preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
##cross-references EMBL:X61708; NID:g32190; CDS_PID:g32191
GENETICS
#gene
GDB:HLA-B
#map_position 6p21.3-6p21.3
#cross-references GDB:120048
CLASSIFICATION
#superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SUMMARY
#length 362 #molecular-weight 40478 #checksum 9585
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qifkntqtdreslnrlgynyqseagsh
99
108
...
1 match found in sequence:
I72113 ; histocompatibility antigen HLA-C alpha chain (allele Cw
(from "PIR 50")
ENTRY
TITLE
histocompatibility antigen HLA-C alpha chain (allele Cw
12022) precursor - human
ORGANISM
#formal_name Homo sapiens #common_name man
#precursor - human
DATE
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
I72113; S32757; S31957
REFERENCE
I56034
#authors
Takiguchi, M.; Nishimura, I.; Hayashi, H.; Karaki, S.;
Kariyone, A.; Kano, K.
J. Immunol. (1989) 143:1372-1378
#journal
#title
The structure and expression of genes encoding serologically
undetected HLA-C locus antigens.
#cross-references MUID:89309827
#accession
I72113
#status
preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-366 #label RES
##cross-references GB:M28172; NID:g187828; CDS_PID:g386906
REFERENCE
S31957
#authors
Vilches, C.
#submission
submitted to the EMBL Data Library, January 1993
#accession
S32757
#molecule_type mRNA
#residues 1-366 #label VIL
##cross-references EMBL:X70856
##note
this allele is designated Cw*12022
GENETICS

```

```

#gene
#cross-references GDB:D6S204
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
                 immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SUMMARY
SEQUENCE #length 366 #molecular-weight 40885 #checksum 4159
Found using 'seq1' (seq1.key)
...
89 qkykrqaqadvrlnrlrgyynqseagsh
99 108
|-----|
...
1 match found in sequence:
A30345 : MHC class I histocompatibility antigen HLA-B51 precursor -
(from 'PIR 50')
ENTRY A30345 #type complete
TITLE MHC class I histocompatibility antigen HLA-B51 precursor -
human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
06-Sep-1996
ACCESSIONS A30345; I68746
REFERENCE A30345
#authors Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
P.; Kano, K.; Takiguchi, M.
#journal J. Immunol. (1989) 142:306-311
#title HLA-B51 and HLA-B*52 differ by only two amino acids which are
in the helical region of the alpha-1 domain.
#cross-references MUID:89080265
#accession A30345
#status preliminary
#molecule_type mRNA
#residues 1-362 #label HAY
REFERENCE I5457
#authors Pohl, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and the
evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68746
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:L41087; NID:g735900; CDS_PID:g735902
GENETICS
#gene GDB:HLA-B
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
                 immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SUMMARY
SEQUENCE #length 362 #molecular-weight 40566 #checksum 9719
Found using 'seq1' (seq1.key)
...
89 qifktntqtenrlrlnryynqseagsh
99 108
|-----|

```

```

1 match found in sequence:
S25536 : MHC class I histocompatibility antigen - rat
(from 'PIR 50')
ENTRY S25536 #type complete
TITLE MHC class I histocompatibility antigen - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
06-Sep-1996
ACCESSIONS I83469; S25536
REFERENCE I60327
#authors Rothermel, E.; Heine, L.; Wurst, W.; Gunther, E.
#journal Immunogenetics (1993) 38:82-91
#title Characterization of a class IB gene of the rat major
histocompatibility complex.
#cross-references MUID:93246303
#accession I83469
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-353 #label RES
#cross-references EMBL:X67504; NID:g56484; CDS_PID:g56485
GENETICS
#note gene name 11/3R
CLASSIFICATION #superfamily class I histocompatibility antigen;
                 immunoglobulin homology
SUMMARY #length 353 #molecular-weight 39874 #checksum 7572
SEQUENCE
Found using 'seq1' (seq1.key)
...
86 rragdehmfvrslrlnrgyynqseagsh
96 105
|-----|
...
1 match found in sequence:
I59308 : class I histocompatibility antigen - pygmy chimpanzee
(from 'PIR 50')
ENTRY I59308 #type fragment
TITLE class I histocompatibility antigen - pygmy chimpanzee
(fragment)
ORGANISM #formal_name Pan paniscus #common_name pygmy chimpanzee,
bonobo
DATE 31-May-1996 #sequence_revision 31-May-1996 #text_change
31-May-1996
ACCESSIONS I59308
REFERENCE I59308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I59308
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-354 #label RES
#cross-references EMBL:U05575; NID:g454767; CDS_PID:g454768
SUMMARY #length 354 #checksum 3211
SEQUENCE
Found using 'seq1' (seq1.key)
...
81 qickaqatdrenrlrlnryynqseagsh
91 100
|-----|

```

```

1 match found in sequence:
I80165 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
ENTRY
TITLE      class I histocompatibility antigen - pygmy chimpanzee
            (fragment)
ORGANISM    #formal_name Pan paniscus #common_name pygmy chimpanzee,
            bonobo
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS  I80165
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80165
            #status      preliminary; translated from GB/EMBL/DBJ
            #molecule_type mRNA
            #residues     1-354 ##label RES
            ##cross-references EMBL:U05576; NID:g454771; CDS_PID:g454770
SUMMARY     #length 354 #checksum 2433
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  qickaaqtdreslgnryyngsagsh
    |-----|
    91      100
...

1 match found in sequence:
I80166 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
ENTRY
TITLE      class I histocompatibility antigen - pygmy chimpanzee
            (fragment)
ORGANISM    #formal_name Pan paniscus #common_name pygmy chimpanzee,
            bonobo
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS  I80166
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80166
            #status      preliminary; translated from GB/EMBL/DBJ
            #molecule_type mRNA
            #residues     1-354 ##label RES
            ##cross-references EMBL:U05577; NID:g454771; CDS_PID:g454772
SUMMARY     #length 354 #checksum 3433
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  qiylkaqtdreslgnryyngsagsh
    |-----|
    91      100
...

1 match found in sequence:
I80167 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
ENTRY
TITLE      class I histocompatibility antigen - chimpanzee (fragment)
            (fragment)
ORGANISM    #formal_name Pan paniscus #common_name pygmy chimpanzee,
            bonobo
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS  I80167
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80167
            #status      preliminary; translated from GB/EMBL/DBJ
            #molecule_type mRNA
            #residues     1-354 ##label RES
            ##cross-references EMBL:U05578; NID:g454773; CDS_PID:g454774
SUMMARY     #length 354 #checksum 3983
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  qickaaqtdrenlralryyngsagsh
    |-----|
    91      100
...

1 match found in sequence:
I80168 ; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
ENTRY
TITLE      class I histocompatibility antigen - chimpanzee (fragment)
            (fragment)
ORGANISM    #formal_name Pan troglodytes #common_name chimpanzee
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS  I80168
REFERENCE    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors    A.L.; Bontrop, R.E.; Watkins, D.I.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80168
            #status      preliminary; translated from GB/EMBL/DBJ
            #molecule_type mRNA
            #residues     1-354 ##label RES
            ##cross-references EMBL:U05579; NID:g454775; CDS_PID:g454776
SUMMARY     #length 354 #checksum 5067
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  rnvkasaqtyrenlralryyngsagsh
    |-----|
    91      100
...

1 match found in sequence:
I80169 ; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
ENTRY
TITLE      class I histocompatibility antigen - chimpanzee (fragment)
            (fragment)
ORGANISM    #formal_name Pan troglodytes #common_name chimpanzee
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change

```

```
ACCESSIONS 180169
REFERENCE 159308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references EMBL:94286544
#accession 180169
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-355 #label RES
##cross-references EMBL:U05580; NID:g454777; CDS_PID:g454778
SUMMARY
SEQUENCE #length 355 #checksum 4603
Found using 'seq1' (seq1.key)
...
81 rmkasaqtdrenlrtrialryynqseagshi
91 100
|-----|
1 match found in sequence:
180171 : class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
ENTRY 180171 #type fragment
TITLE class I histocompatibility antigen - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996
ACCESSIONS 180171
REFERENCE 159308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references EMBL:94286544
#accession 180171
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-355 #label RES
##cross-references EMBL:U05582; NID:g454781; CDS_PID:g454782
SUMMARY
SEQUENCE #length 355 #checksum 6021
Found using 'seq1' (seq1.key)
...
81 rmkasaqtdrenlrtrialryynqseagsh
91 100
|-----|
1 match found in sequence:
180175 : class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
ENTRY 180175 #type fragment
TITLE class I histocompatibility antigen - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996
ACCESSIONS 180175
REFERENCE 159308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references EMBL:94286544
```

```
#accession 180175
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-137 #label RES
##cross-references EMBL:U05586; NID:g454789; CDS_PID:g454790
SUMMARY
SEQUENCE #length 137 #checksum 5336
Found using 'seq1' (seq1.key)
...
30 qiykaqatdrvslgnlrqyynqseagsh
40 49
|-----|
1 match found in sequence:
136957 : MHC ChIA chain - chimpanzee
(from "PIR 50")
ENTRY 136957 #type complete
TITLE MHC ChIA chain - chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
13-Sep-1996
ACCESSIONS 136957
REFERENCE 136956
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession 136957
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-363 #label RES
##cross-references GB:M24045; NID:gl76814; CDS_PID:gl76815
SUMMARY
SEQUENCE #length 363 #molecular_weight 40540 #checksum 610
Found using 'seq1' (seq1.key)
...
89 rnvkasaqtdrenlrtrialryynqseagsh
99 108
|-----|
1 match found in sequence:
136956 : MHC ChIA chain - chimpanzee (fragment)
(from "PIR 50")
ENTRY 136956 #type fragment
TITLE MHC ChIA chain - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
13-Sep-1996
ACCESSIONS 136956
REFERENCE 136956
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession 136956
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-308 #label RES
##cross-references GB:M24044; NID:gl76812; CDS_PID:gl76813
SUMMARY
SEQUENCE #length 308 #checksum 7529
Found using 'seq1' (seq1.key)
```

```
...
35 qisktnaqtyreslnrlrgyynqseagshi
    45
    |-----|
    54
...
1 match found in sequence:
I36958 ; MHC ChIA chain - chimpanzee (fragment)
ENTRY (from "PIR 50")
TITLE MHC ChIA chain - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
13-Sep-1996
ACCESSIONS I36958
REFERENCE I36956
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I36958
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-313 #label RES
#cross-references GB:M24046; NID:g176816; CDS_PID:g176817
SUMMARY #length 313 #checksum 5311
SEQUENCE
Found using 'seq1' (seq1.key)
...
36 qkykraqadrvslrlrgyynqseagsh
    46
    |-----|
    55
...
1 match found in sequence:
I68701 ; cell surface antigen - human (fragment)
ENTRY (from "PIR 50")
TITLE cell surface antigen - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
15-Jun-1996
ACCESSIONS I68701
REFERENCE I54412
#authors Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
#journal Immunogenetics (1984) 20:237-252
#title Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
#cross-references MUID:84287690
#accession I68701
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-300 #label RES
#cross-references GB:M27540; NID:g187733; CDS_PID:g386890
SUMMARY #length 300 #checksum 294
SEQUENCE
Found using 'seq1' (seq1.key)
...
27 qiykahagtdreslnrlrgyynqseagsh
    37
    |-----|
    46
...
1 match found in sequence:
I62045 ; gene HLA B-1517 protein - human
ENTRY (from "PIR 50")
TITLE gene HLA B-1517 protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
13-Sep-1996
ACCESSIONS I62045
REFERENCE I38421
#authors Hilgebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.; Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B*15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62045
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references EMBL:U01848; NID:g402676; CDS_PID:g402677
GENETICS
#note gene name HLA B-1517
SUMMARY #length 362 #molecular-weight 40417 #checksum 7730
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 rnmkasaqtyreslnrlrgyynqseagsh
    99
    |-----|
    108
...
1 match found in sequence:
I54298 ; gene HLA-B protein - human
ENTRY (from "PIR 50")
TITLE gene HLA-B protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
ACCESSIONS I54298
REFERENCE I54298
#authors Chertkoff, L.P.; Herrera, M.; Fainboim, L.; Satz, M.L.
#journal Hum. Immunol. (1991) 31:153-158
#title Complete nucleotide sequence of a genomic clone encoding HLA-B*35 isolated from a Caucasian individual of Hispanic origin. Identification of a new variant of HLA-B*35.
#cross-references MUID:91365651
#accession I54298
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M63454; NID:g187856; CDS_PID:g403145
GENETICS
#note 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
#introns gene name HLA-B
SUMMARY #length 362 #molecular-weight 40564 #checksum 567
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qifktnqtyreslnrlrgyynqseagshi
    99
    |-----|
    108
...
1 match found in sequence:
I54298 ; gene HLA-B protein - human
ENTRY (from "PIR 50")
TITLE gene HLA-B protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
ACCESSIONS I54298
REFERENCE I54298
#authors Chertkoff, L.P.; Herrera, M.; Fainboim, L.; Satz, M.L.
#journal Hum. Immunol. (1991) 31:153-158
#title Complete nucleotide sequence of a genomic clone encoding HLA-B*35 isolated from a Caucasian individual of Hispanic origin. Identification of a new variant of HLA-B*35.
#cross-references MUID:91365651
#accession I54298
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M63454; NID:g187856; CDS_PID:g403145
GENETICS
#note 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
#introns gene name HLA-B
SUMMARY #length 362 #molecular-weight 40564 #checksum 567
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qifktnqtyreslnrlrgyynqseagshi
    99
    |-----|
    108
...
```

```

-----
1 match found in sequence:
I56034 ; gene HLA-C protein - human
ENTRY (from "PIR 50") I56034 #type complete
TITLE gene HLA-C protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56034
REFERENCE Takiguchi, M.; Nishimura, I.; Hayashi, H.; Karaki, S.;
#authors Kariyone, A.; Kano, K.
#journal J. Immunol. (1989) 143:1372-1378
#title The structure and expression of genes encoding serologically
undetected HLA-C locus antigens.
#cross-references MUID:89309827
#accession I56034 preliminary; translated from GB/EMBL/DBJ
#status #molecule_type DNA
#residues 1-366 #label RES
#cross-references GB:M28171; NID:q187826; CDS_PID:g385905
SUMMARY #length 366 #molecular-weight 40855 #checksum 5205
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qkykrqatqdrvsirlnryngseagsh
99 108
-----
1 match found in sequence:
I38437 ; HLA B-40011 - human
ENTRY (from "PIR 50") I38437 #type complete
TITLE HLA B-40011 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I38437
REFERENCE Ways, J.W.; Lawlor, D.A.; Wan, A.M.; Parham, P.
#authors Immunogenetics (1987) 25:323-328
#journal A Transposable Epitope of HLA-B7, B40 Molecules.
#title #cross-references MUID:87192942
#accession I38437
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references EMBL:U03698; NID:g425708; CDS_PID:g425709
SUMMARY #length 362 #molecular-weight 40432 #checksum 8017
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qiskntqtqyreslrnryngseagsh
99 108
-----
1 match found in sequence:
I54493 ; HLA-A protein - human
ENTRY (from "PIR 50") I54493 #type complete
TITLE HLA-A protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-May-1995 #sequence_revision 21-Jul-1995 #text_change
ACCESSIONS I54493
REFERENCE S52486
#authors Herrera, M.J.

```

```

ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I54493
REFERENCE Little, A.M.; Madrigal, J.A.; Parham, P.
#authors Immunogenetics (1992) 35:41-45
#journal Molecular definition of an elusive third HLA-A9 molecule:
#title HLA-A9.3
#cross-references MUID:92104637
#accession I54493 preliminary; translated from GB/EMBL/DBJ
#status #molecule_type DNA
#residues 1-365 #label RES
#cross-references GB:M64741; NID:q187615; CDS_PID:q187616
SUMMARY #length 365 #molecular-weight 40831 #checksum 2547
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 gkvkahsqtdrenlrlnryngseagsh
99 108
-----
1 match found in sequence:
I54416 ; HLA-AW24 protein - human
ENTRY (from "PIR 50") I54416 #type complete
TITLE HLA-AW24 protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I54416
REFERENCE N'Guyen, C.; Sodoyer, R.; Trucy, J.; Strachan, T.; Jordan,
#authors B.R.
#journal Immunogenetics (1985) 21:479-489
#title The HLA-AW24 gene: sequence, surroundings and comparison with
#cross-references MUID:85206128
#accession I54416
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-365 #label RES
#cross-references GB:M15497; NID:q187644; CDS_PID:g386877
SUMMARY #length 365 #molecular-weight 40644 #checksum 1573
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 gkvkahsqtdrenlrlnryngseagsh
99 108
-----
1 match found in sequence:
S52486 ; HLA-B protein alpha chain - human
ENTRY (from "PIR 50") S52486 #type complete
TITLE HLA-B protein alpha chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-May-1995 #sequence_revision 21-Jul-1995 #text_change
ACCESSIONS S52486
REFERENCE S52486
#authors Herrera, M.J.

```

```
#submission submitted to the EMBL Data Library, February 1995
#accession S52486
##status preliminary
##molecule_type mRNA
##residues 1-362 #label HER
##cross-references EMBL:X84725
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SEQUENCE
#length 362 #molecular-weight 40592 #checksum 651
Found using 'seq1' (seq1.key)
```

```
...
89 giskntqtyreslnrlrgyynqseagsh
99
108
```

```
-----
1 match found in sequence:
I62044 ; HLA-B*1514 - human
(from "PIR 50")
ENTRY I62044 #type complete
TITLE HLA-B*1514 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I62044
REFERENCE I38421
#authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bisio, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B*15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62044
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:L19937; NID:g493167; CDS_PID:g493168
GENETICS
#note gene name HLA-B
#length 362 #molecular-weight 40289 #checksum 9607
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
89 giskntqtyreslnrlrgyynqseagsh
99
108
```

```
-----
1 match found in sequence:
I56130 ; HLA-B*5401 - human
(from "PIR 50")
ENTRY I56130 #type complete
TITLE HLA-B*5401 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56130
REFERENCE I56130
#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal J. Immunol. (1992) 148:1155-1162
#title HLA-B*22: a family of molecules with identity to HLA-B7 in
the alpha 1-helix.
#cross-references MUID:92148136
```

```
#accession I56130
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:M77774; NID:g184116; CDS_PID:g184117
SUMMARY
SEQUENCE
#length 362 #molecular-weight 40380 #checksum 8309
Found using 'seq1' (seq1.key)
```

```
...
89 gikyqaqtdreslnrlrgyynqseagsh
99
108
```

```
-----
1 match found in sequence:
I72752 ; HLA-B*5501 - human
(from "PIR 50")
ENTRY I72752 #type complete
TITLE HLA-B*5501 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I72752
REFERENCE I56130
#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal J. Immunol. (1992) 148:1155-1162
#title HLA-B*22: a family of molecules with identity to HLA-B7 in
the alpha 1-helix.
#cross-references MUID:92148136
#accession I72752
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:M77778; NID:g184118; CDS_PID:g184119
SUMMARY
SEQUENCE
#length 362 #molecular-weight 40496 #checksum 7953
Found using 'seq1' (seq1.key)
```

```
...
89 gikyqaqtdreslnrlrgyynqseagsh
99
108
```

```
-----
1 match found in sequence:
I72753 ; HLA-B*5502 - human
(from "PIR 50")
ENTRY I72753 #type complete
TITLE HLA-B*5502 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I72753
REFERENCE I56130
#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal J. Immunol. (1992) 148:1155-1162
#title HLA-B*22: a family of molecules with identity to HLA-B7 in
the alpha 1-helix.
#cross-references MUID:92148136
#accession I72753
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:M77779; NID:g184120; CDS_PID:g184121
SUMMARY
SEQUENCE
#length 362 #molecular-weight 40466 #checksum 8038
```

Found using 'seq1' (seq1.key)

```
...
-----|-----|
89  qiylkaqatdreslnrlrgyynqseagsh
    (from "PIR 50")
    99 108
```

```
-----
1 match found in sequence:
172754 ; HLA-B*5601 - human
    (from "PIR 50")
ENTRY      I72754      #type complete
TITLE      HLA-B*5601 - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I72754
REFERENCE   I56130
#authors    Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal     J. Immunol. (1992) 148:1155-1162
#title       HLA-B*22: a family of molecules with identity to HLA-B7 in
              the alpha 1-helix.
#cross-references MUID:92148136
#accession   I72754
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues   1-362 ##label RES
##cross-references GB:M7776; NID:g184122; CDS_PID:g184123
SUMMARY      #length 362 #molecular-weight 40478 #checksum 7910
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
-----|-----|
89  qiylkaqatdreslnrlrgyynqseagsh
    (from "PIR 50")
    99 108
```

```
-----
1 match found in sequence:
172755 ; HLA-B*5602 - human
    (from "PIR 50")
ENTRY      I72755      #type complete
TITLE      HLA-B*5602 - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I72755
REFERENCE   I56130
#authors    Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal     J. Immunol. (1992) 148:1155-1162
#title       HLA-B*22: a family of molecules with identity to HLA-B7 in
              the alpha 1-helix.
#cross-references MUID:92148136
#accession   I72755
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues   1-362 ##label RES
##cross-references GB:M7775; NID:g184124; CDS_PID:g184125
SUMMARY      #length 362 #molecular-weight 40460 #checksum 7841
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
-----|-----|
89  qiylkaqatdreslnrlrgyynqseagsh
    (from "PIR 50")
    99 108
```

```
...
-----
1 match found in sequence:
159645 ; HLA-B-6701 - human
    (from "PIR 50")
ENTRY      I59645      #type complete
TITLE      HLA-B-6701 - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I59645
REFERENCE   I59645
#authors    Little, A.M.; Domena, J.D.; Hildebrand, W.H.; Shen, S.Y.;
              Barber, L.D.; Marsh, S.G.; Bias, W.B.; Parham, P.
#journal     Tissue Antigens (1994) 43:38-43
#title       HLA-B*67: a member of the HLA-B16 family that expresses the
              ME1 epitope.
#cross-references MUID:94294981
#accession   I59645
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues   1-362 ##label RES
##cross-references GB:I17005; NID:g292147; CDS_PID:g488426
SUMMARY      #length 362 #molecular-weight 40342 #checksum 9311
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
-----|-----|
89  qiylkaqatdreslnrlrgyynqseagsh
    (from "PIR 50")
    99 108
```

```
-----
1 match found in sequence:
137521 ; HLA-B*57.2 antigen - human
    (from "PIR 50")
ENTRY      I37521      #type complete
TITLE      HLA-B*57.2 antigen - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I37521
REFERENCE   I37476
#authors    Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,
              R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
              Petzl-Erler, M.L.; Du Toit, E.D.; Parham, P.
#journal     J. Immunol. (1992) 149:3411-3415
#title       Distinctive HLA-A,B antigens of black populations formed by
              interallelic conversion.
#cross-references MUID:93056508
#accession   I37521
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues   1-362 ##label RES
##cross-references EMBL:X61707; NID:g32186; CDS_PID:g32187
SUMMARY      #length 362 #molecular-weight 40342 #checksum 7369
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
-----|-----|
89  rnmkasadyrenlralryynqseagshi
    (from "PIR 50")
    99 108
```

```

1 match found in sequence:
I54430 ; HLA-Cw1 heavy chain - human
ENTRY      I54430      #type complete
TITLE      HLA-Cw1 heavy chain - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I54430
REFERENCE- #authors
#journal   Gussow, D.; Rein, R.S.; Meijer, I.; de Hoog, W.; Seemann,
#title     G.H.; Hochstenbach, F.M.; Ploegh, H.L.
           Isolation, expression, and the primary structure of HLA-Cw1
           and HLA-Cw2 genes: evolutionary aspects [published erratum
           appears in Immunogenetics 1988;27(2):158].
#cross-references MUID:87192941
#accession I54430      preliminary; translated from GB/EMBL/DBJ
#status    #molecule_type DNA
#residues  1-366 #label RES
#cross-references GB:M16272; NID:g187913; CDS_PID:g386912
SUMMARY    #length 366 #molecular-weight 40936 #checksum 5559
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  qkykrqatdrvslrnlrgyynqseagsh
99  108
-----|-----|
1 match found in sequence:
I54505 ; lymphocyte antigen - human
ENTRY      I54505      #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I54505
REFERENCE- #authors
#journal   Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.;
#title     Juji, T.; Kano, K.; Takiguchi, M.
           Immunogenetics (1993) 37:212-216
           Molecular analysis of HLA-B39 subtypes.
#cross-references MUID:93131294
#accession I54505      preliminary; translated from GB/EMBL/DBJ
#status    #molecule_type DNA
#residues  1-362 #label RES
#cross-references GB:M94052; NID:g184163; CDS_PID:g184164
SUMMARY    #length 362 #molecular-weight 40328 #checksum 9858
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  qickntqtdreslrlrnlrgyynqseagsh
99  108
-----|-----|
1 match found in sequence:
I56149 ; lymphocyte antigen - human
ENTRY      I56149      #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I56149
REFERENCE- #authors
#journal   Hildebrand, W.H.; Madrigal, J.A.; Bellich, M.P.; Zemmour, J.;
#title     Ward, F.E.; Williams, R.C.; Parham, P.
           J. Immunol. (1992) 149:3563-3568
           Serologic cross-reactivities poorly reflect allelic
           relationships in the HLA-B*12 and HLA-B*21 groups. Dominant
           epitopes of the alpha 2 helix.
#cross-references MUID:93056529
#accession I56149      preliminary; translated from GB/EMBL/DBJ
#status    #molecule_type mRNA
#residues  1-362 #label RES
#cross-references GB:M84694; NID:g188474; CDS_PID:g188475
SUMMARY    #length 362 #molecular-weight 40519 #checksum 616
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  qiskntqtgyreslrlrnlrgyynqseagsh
99  108
-----|-----|
1 match found in sequence:
I59622 ; lymphocyte antigen - human
ENTRY      I59622      #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I59622
REFERENCE- #authors
#journal   Zemmour, J.; Gumperz, J.E.; Hildebrand, W.H.; Ward, F.E.;
#title     Marsh, S.G.; Williams, R.C.; Parham, P.
           Tissue Antigens (1992) 39:249-257
           The molecular basis for reactivity of anti-Cw1 and anti-Cw3
           alloantisera with HLA-B*46 haplotypes.
#cross-references MUID:93031775
#accession I59622      preliminary; translated from GB/EMBL/DBJ
#status    #molecule_type mRNA
#residues  1-366 #label RES
#cross-references GB:M84171; NID:g187862; CDS_PID:g187863
GENETICS
#note      gene name HLA-C
SUMMARY    #length 366 #molecular-weight 40950 #checksum 5590
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  qkykrqatdrvslrnlrnlrgyynqseagsh
99  108
-----|-----|
1 match found in sequence:
I59651 ; lymphocyte antigen - human
ENTRY      I59651      #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change

```

```
02-Jul-1996
ACCESSIONS 159651
REFERENCE 159651
#authors Arnett, K.L.; Adams, E.J.; Domena, J.D.; Parham, P.
#journal Tissue Antigens (1994) 44:318-321
#title Structure of a novel subtype of B7 (B*0705) isolated from a
Chinese individual.
#cross-references MUID:95184211
#accession 159651
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:I33922; NID:g520834; CDS_PID:g520835
SUMMARY #length 362 #molecular-weight 40473 #checksum 8201
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qiykaqtdreslnrlrgyynqseagsh
99 108
|-----|

1 match found in sequence:
159655 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I59655 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS 159655
REFERENCE Adams, E.J.; Little, A.
#authors Tissue Antigens (1995) 46:204-205
#journal Identification of a novel HLA-B allele (B*4008) in a patient
#title with leukemia.
#accession 159655
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:I41353; NID:gl041064; CDS_PID:gl041065
GENETICS
#note gene name HLA-B*4008
SUMMARY #length 362 #molecular-weight 40550 #checksum 417
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qifktntqtyreslnrlrgyynqseagsh
99 108
|-----|

1 match found in sequence:
159655 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I59655 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS 159655
REFERENCE Bellich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
#authors Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#journal Nature (1992) 357:326-329
```

```
Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession 161903
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:M84380; NID:gl87707; CDS_PID:gl87708
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40362 #checksum 286
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qfktntqtyreslnrlrgyynqseagsh
99 108
|-----|

1 match found in sequence:
161904 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I61904 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS 161904
REFERENCE Bellich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
#authors Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#journal Nature (1992) 357:326-329
#title Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession 161904
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:M84381; NID:gl87711; CDS_PID:gl87712
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40514 #checksum 187
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qfktntqtyreslnrlrgyynqseagshi
99 108
|-----|

1 match found in sequence:
161905 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I61905 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS 161905
REFERENCE Bellich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
#authors Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#journal Nature (1992) 357:326-329
#title Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession 161905
```

```

##status      preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues    1-362 ##label RES
##cross-references GB:M84383; NID:g187715; CDS_PID:g187716
GENETICS
#note
SUMMARY      gene name HLA-B
SEQUENCE     #length 362 #molecular-weight 40430 #checksum 193
Found using 'seq1' (seq1.key)
...
89  qiskntqttyreslnrlrgyynqseagsh
    |-----|
    99 108
...
1 match found in sequence:
161906 : lymphocyte antigen - human
(from "PIR 50")
ENTRY      I61906 #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I61906
REFERENCE   I37120
#authors   Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
           Williams, R.C.; Luz, R.; Petz1-Erlor, M.L.; Parham, P.
#journal   Nature (1992) 357:326-329
#title     Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession I61906
##status   preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:M84384; NID:g187717; CDS_PID:g187718
GENETICS
#note
SUMMARY     gene name HLA-B
SEQUENCE    #length 362 #molecular-weight 40600 #checksum 393
Found using 'seq1' (seq1.key)
...
89  qiskntqttyreslnrlrgyynqseagsh
    |-----|
    99 108
...
1 match found in sequence:
161907 : lymphocyte antigen - human
(from "PIR 50")
ENTRY      I61907 #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I61907
REFERENCE   I37120
#authors   Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
           Williams, R.C.; Luz, R.; Petz1-Erlor, M.L.; Parham, P.
#journal   Nature (1992) 357:326-329
#title     Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession I61907
##status   preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-362 ##label RES

```

```

##cross-references GB:M84385; NID:g187719; CDS_PID:g187720
GENETICS
#note
SUMMARY     gene name HLA-B
SEQUENCE    #length 362 #molecular-weight 40374 #checksum 351
Found using 'seq1' (seq1.key)
...
89  qifkntqttyreslnrlrgyynqseagsh
    |-----|
    99 108
...
1 match found in sequence:
168850 : lymphocyte antigen - human
(from "PIR 50")
ENTRY      I68850 #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I68850
REFERENCE   I54505
#authors   Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.;
           Juji, T.; Kano, K.; Takiguchi, M.
#journal   Immunogenetics (1993) 37:212-216
#title     Molecular analysis of HLA-B39 subtypes.
#cross-references MUID:93131294
#accession I68850
##status   preliminary; translated from GB/EMBL/DBDJ
##molecule_type DNA
##residues 1-362 ##label RES
##cross-references GB:M94053; NID:g184165; CDS_PID:g184166
SUMMARY     gene name HLA-B
SEQUENCE    #length 362 #molecular-weight 40327 #checksum 132
Found using 'seq1' (seq1.key)
...
89  qiskntqttdreslnrlrgyynqseagsh
    |-----|
    99 108
...
1 match found in sequence:
181231 : lymphocyte antigen - human
(from "PIR 50")
ENTRY      I81231 #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I81231
REFERENCE   I59622
#authors   Zemmour, J.; Gumperz, J.E.; Hildebrand, W.H.; Ward, F.E.;
           Marsh, S.G.; Williams, R.C.; Parham, P.
#journal   Tissue Antigens (1992) 39:249-257
#title     The molecular basis for reactivity of anti-Cw1 and anti-Cw3
           .. alloantisera with HLA-B46 haplotypes.
##cross-references MUID:93031775
#accession I81231
##status   preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-366 ##label RES
##cross-references GB:M84172; NID:g187864; CDS_PID:g187865
GENETICS
#note
SUMMARY     gene name HLA-C
           #length 366 #molecular-weight 40784 #checksum 5046

```

SEQUENCE

Found using 'seq1' (seq1.key)

...

89 qkykrqatdrvslnrlrgyynqseagsh
99 108
|-----|

...

1 match found in sequence:

I81232 ; lymphocyte antigen - human
(from "PIR 50")
ENTRY I81232 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I81232
REFERENCE I59622
#authors Zemmour, J.; Gumperz, J.E.; Hildebrand, W.H.; Ward, F.E.;
Marsh, S.G.; Williams, R.C.; Parham, P.
#journal Tissue Antigens (1992) 39:249-257
#title The molecular basis for reactivity of anti-Cw1 and anti-Cw3
alloantisera with HLA-B46 haplotypes.
#cross-references MUID:93031775
#accession I81232 preliminary; translated from GB/EMBL/DBJ
#status
#molecule_type mRNA
#residues 1-366 #label RES
#cross-references GB:M84174; NID:g187868; CDS_PID:g187869

GENETICS

#note gene name HLA-C

SUMMARY #length 366 #molecular-weight 40772 #checksum 5003

SEQUENCE

Found using 'seq1' (seq1.key)

...

89 qkykrqatdrvslnrlrgyynqseagsh
99 108
|-----|

...

1 match found in sequence:

I81233 ; lymphocyte antigen - human
(from "PIR 50")
ENTRY I81233 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I81233
REFERENCE I59631
#authors Theller, G.; Pando, M.; Delfino, J.M.; Takiguchi, M.; Satz,
M.L.
#journal Tissue Antigens (1993) 41:143-147
#title Isolation and characterization of two new functional subtypes
of HLA-B35.
#cross-references MUID:93303752
#accession I81233 preliminary; translated from GB/EMBL/DBJ
#status
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:L04695; NID:g187892; CDS_PID:g187893

GENETICS

#note gene name HLA-B

SUMMARY #length 362 #molecular-weight 40497 #checksum 885

SEQUENCE

Found using 'seq1' (seq1.key)

...

89 qifkntqtqreslnrlrgyynqseagsh
99 108
|-----|

...

1 match found in sequence:

I81239 ; lymphocyte antigen - human
(from "PIR 50")
ENTRY I81239 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I81239
REFERENCE I59645
#authors Little, A.M.; Domena, J.D.; Hildebrand, W.H.; Shen, S.Y.;
Barber, L.D.; Marsh, S.G.; Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:38-43
#title HLA-B*67: a member of the HLA-B16 family that expresses the
ME1 epitope.
#cross-references MUID:94294981
#accession I81239 preliminary; translated from GB/EMBL/DBJ
#status
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:L41628; NID:g773174; CDS_PID:g773175

GENETICS

#note gene name HLA-B*40012

SUMMARY #length 362 #molecular-weight 40432 #checksum 8017

SEQUENCE

Found using 'seq1' (seq1.key)

...

89 qiskntqtqreslnrlrgyynqseagsh
99 108
|-----|

...

1 match found in sequence:

I84488 ; lymphocyte antigen - human
(from "PIR 50")
ENTRY I84488 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I84488
REFERENCE I38464
#authors Adams, E.J.; Martinez-Naves, E.; Arnett, K.L.; Little, A.M.;
Ryan, D.B.; Parham, P.
#journal Tissue Antigens (1995) 45:18-26
#title HLA-B16 antigens: sequence of the ST-16 antigen, further
definition of two B38 subtypes and evidence for convergent
evolution of B*3902.
#cross-references MUID:95242308
#accession I84488 preliminary; translated from GB/EMBL/DBJ
#status
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:L36318; NID:g793946; CDS_PID:g793947

GENETICS

#note gene name HLA-B-3905

SUMMARY #length 362 #molecular-weight 40376 #checksum 719

SEQUENCE

Found using 'seq1' (seq1.key)

```
...
89  qickntqtyreslnrlrgyynqseagsh
    |-----|
    99  108
...

```

```
-----
1 match found in sequence:
I84490 : lymphocyte antigen - human
(from "PIR 50")
ENTRY      I84490      #type complete
TITLE      lymphocyte antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I84490
REFERENCE   I38518
#authors   Browning, M.J.; Madrigal, J.A.; Krausa, P.; Kowalski, H.;
            Allsopp, C.E.; Little, A.M.; Turner, S.; Adams, E.J.;
            Arnett, K.L.; Bodmer, W.F.; Bodmer, J.G.; Parham, P.
#journal   Tissue Antigens (1995) 45:177-187
#title     The HLA-A,B,C genotype of the class I negative cell line
            Daudi reveals novel HLA-A and -B alleles.
#cross-references MUID:95282145
#accession  I84490
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-362 #label RES
#cross-references GB:I33923; NID:g520836; CDS_PID:g520837
GENETICS
#note      gene name HLA-A10-B38
SUMMARY    #length 362 #molecular-weight 40355 #checksum 8277
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```
89  rmkasaqtyreslnrlrgyynqseagsh
    |-----|
    99  108
...

```

```
-----
1 match found in sequence:
I59654 : major histocompatibility complex class I - human
(from "PIR 50")
ENTRY      I59654      #type complete
TITLE      major histocompatibility complex class I - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I59654
REFERENCE   I59654
#authors   Liener, K.; McCluskey, J.; Bennett, G.; Fowler, C.; Russ, G.
#journal   Tissue Antigens (1995) 45:12-17
#title     HLA class I variation in Australian aborigines:
            characterization of allele B*1521.
#cross-references MUID:95242307
#accession  I59654
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-362 #label RES
#cross-references GB:I32862; NID:g487817; CDS_PID:g487818
GENETICS
#note      gene name HLA-B
SUMMARY    #length 362 #molecular-weight 40354 #checksum 9646
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```
...
89  qickntqtyreslnrlrgyynqseagsh
    |-----|
    99  108
...

```

```
-----
1 match found in sequence:
I37120 : MCH class I HLA-B*5104 - human
(from "PIR 50")
ENTRY      I37120      #type complete
TITLE      MCH class I HLA-B*5104 - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
ACCESSIONS I37120
REFERENCE   I37120
#authors   Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
            Williams, R.C.; Luz, R.; Petzi-Erler, M.L.; Parham, P.
#journal   Nature (1992) 357:326-329
#title     Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession  I37120
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-362 #label RES
#cross-references EMBL:Z15143; NID:g28234; CDS_PID:g28235
SUMMARY    #length 362 #molecular-weight 40560 #checksum 9591
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```
89  qifkntqtyreslnrlrgyynqseagsh
    |-----|
    99  108
...

```

```
-----
1 match found in sequence:
I79640 : MHC cell surface antigen - human (fragment)
(from "PIR 50")
ENTRY      I79640      #type fragment
TITLE      MHC cell surface antigen - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I79640
REFERENCE   I59188
#authors   Bronson, S.K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.;
            Geraghty, D.E.; Chaplin, D.D.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1991) 88:1676-1680
#title     Isolation and characterization of yeast artificial chromosome
            clones linking the HLA-B and HLA-C loci.
#cross-references MUID:91156671
#accession  I79640
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues  1-181 #label RES
#cross-references GB:M59865; NID:g187802; CDS_PID:g187803
GENETICS
#introns   90/1
#note      gene name HLA-C
SUMMARY    #length 181 #checksum 2853
SEQUENCE
Found using 'seq1' (seq1.key)
...

```



```

30  qifkntqtyreslnrlrgyynqseqsht
    40
    49
    1 match found in sequence:
    13874 : MHC class I antigen - human (fragment)
    (from "PIR 50")
    ENTRY      I38874      #type fragment
    TITLE      MHC class I antigen - human (fragment)
    ORGANISM    #formal_name Homo sapiens #common_name man
    DATE        07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
    15-Jun-1996
    ACCESSIONS I38874
    REFERENCE   I38860
    #authors    Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.;
    #journal     Rickards, O.; De Stefano, G.; Watkins, D.I.
    #title       HLA-B alleles of the Cayapa of Ecuador: new B39 and B15
    #cross-references MIM:95317819
    #accession    I38874
    #status      preliminary; translated from GB/EMBL/DBJ
    #molecule_type DNA
    #residues    1-137 #label RES
    ##cross-references EMBL:U15638; NID:g930330; CDS_PID:g930331
    SUMMARY
    SEQUENCE
    Found using 'seq1' (seq1.key)
    ...

30  qickntqtyreslnrlrgyynqseqsht
    40
    49
    1 match found in sequence:
    138505 : MHC class I histocompatibility antigen - human
    (from "PIR 50")
    ENTRY      I38505      #type complete
    TITLE      MHC class I histocompatibility antigen - human
    ORGANISM    #formal_name Homo sapiens #common_name man
    DATE        06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
    06-Sep-1996
    ACCESSIONS I38505
    REFERENCE   I38505
    #authors    Cerib, N.; Choi, J.W.; Lee, S.; Maye, P.; Kong, Y.; Yang,
    #journal     S.Y.
    #title       Tissue Antigens (1994) 44:193-195
    #cross-references MIM:95141286
    #accession    I38505
    #status      preliminary; translated from GB/EMBL/DBJ
    #molecule_type mRNA
    #residues    1-366 #label RES
    ##cross-references EMBL:U06487; NID:g600483; CDS_PID:g600484
    GENETICS
    #note        gene name HLA-Cw
    SUMMARY      #length 366 #molecular-weight 40855 #checksum 5814
    SEQUENCE
    Found using 'seq1' (seq1.key)
    ...

89  qkykrqatdrvslrnlrgyynqseqsht
    99
    108
    1 match found in sequence:

```

```

30  qifkntqtyreslnrlrgyynqseqsht
    40
    49
    1 match found in sequence:
    13874 : MHC class I antigen - human (fragment)
    (from "PIR 50")
    ENTRY      I38874      #type fragment
    TITLE      MHC class I antigen - human (fragment)
    ORGANISM    #formal_name Homo sapiens #common_name man
    DATE        07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
    15-Jun-1996
    ACCESSIONS I38874
    REFERENCE   I38860
    #authors    Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.;
    #journal     Rickards, O.; De Stefano, G.; Watkins, D.I.
    #title       HLA-B alleles of the Cayapa of Ecuador: new B39 and B15
    #cross-references MIM:95317819
    #accession    I38874
    #status      preliminary; translated from GB/EMBL/DBJ
    #molecule_type DNA
    #residues    1-137 #label RES
    ##cross-references EMBL:U15638; NID:g930330; CDS_PID:g930331
    SUMMARY
    SEQUENCE
    Found using 'seq1' (seq1.key)
    ...

30  qickntqtyreslnrlrgyynqseqsht
    40
    49
    1 match found in sequence:
    13875 : MHC class I antigen - human (fragment)
    (from "PIR 50")
    ENTRY      I38875      #type fragment
    TITLE      MHC class I antigen - human (fragment)
    ORGANISM    #formal_name Homo sapiens #common_name man
    DATE        07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
    15-Jun-1996
    ACCESSIONS I38875
    REFERENCE   I38860
    #authors    Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.;
    #journal     Rickards, O.; De Stefano, G.; Watkins, D.I.
    #title       Immunogenetics (1995) 42:19-27
    #cross-references MIM:95317819
    #accession    I38875
    #status      preliminary; translated from GB/EMBL/DBJ
    #molecule_type DNA
    #residues    1-137 #label RES
    ##cross-references EMBL:U15639; NID:g930332; CDS_PID:g930333
    SUMMARY
    SEQUENCE
    Found using 'seq1' (seq1.key)
    ...

30  qickntqtdreslnrlrgyynqseqsht
    40
    49
    1 match found in sequence:

```

```

I38507 ; MHC class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      I38507      #type complete
TITLE      MHC class I histocompatibility antigen - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS  I38507
REFERENCE    I38505
#authors    Cereb, N.; Choi, J.W.; Lee, S.; Maye, P.; Kong, Y.; Yang, S.Y.
#journal     Tissue Antigens (1994) 44:193-195
#title       Identification of two new HLA-C alleles, Cw*1203 and Cw*1402,
              from the sequence analysis of seven HLA homozygous cell
              lines carrying HLA-C blank.
#cross-references MUID:95141286
#accession   I38507      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    1-366 #label RES
#cross-references EMBL:U06695; NID:g469540; CDS_PID:g469541
GENETICS
#note        gene name HLA-Cw
SUMMARY      #length 366 #molecular-weight 40915 #checksum 4194
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qkykrqagadrslrnlrgyngseagsht
      |-----|
      99      108
...
1 match found in sequence:
I38508 ; MHC class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      I38508      #type complete
TITLE      MHC class I histocompatibility antigen - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS  I38508
REFERENCE    I38505
#authors    Cereb, N.; Choi, J.W.; Lee, S.; Maye, P.; Kong, Y.; Yang, S.Y.
#journal     Tissue Antigens (1994) 44:193-195
#title       Identification of two new HLA-C alleles, Cw*1203 and Cw*1402,
              from the sequence analysis of seven HLA homozygous cell
              lines carrying HLA-C blank.
#cross-references MUID:95141286
#accession   I38508      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    1-366 #label RES
#cross-references EMBL:U06696; NID:g469542; CDS_PID:g469543
GENETICS
#note        gene name HLA-Cw
SUMMARY      #length 366 #molecular-weight 40915 #checksum 4194
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qkykrqagadrslrnlrgyngseagsht
      |-----|
      99      108
...

```

```

1 match found in sequence:
I38509 ; MHC class I histocompatibility antigen - human (fragment)
(from "PIR 50")
ENTRY      I38509      #type fragment
TITLE      MHC class I histocompatibility antigen - human (fragment)
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS  I38509
REFERENCE    I38509
#authors    Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
#journal     Tissue Antigens (1994) 44:271-273
#title       HLA-B*5105, a newly identified B51 IEF variant.
#cross-references MUID:95176331
#accession   I38509      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    1-273 #label RES
#cross-references EMBL:U06697; NID:g469544; CDS_PID:g469545
GENETICS
#note        gene name HLA-B
SUMMARY      #length 273 #checksum 6533
SEQUENCE
Found using 'seq1' (seq1.key)
...
64  qifkntqtyrenlrnlrgyngseagsht
      |-----|
      74      83
...
1 match found in sequence:
I56065 ; MHC class I HLA-B - human
(from "PIR 50")
ENTRY      I56065      #type complete
TITLE      MHC class I HLA-B - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS  I56065
REFERENCE    I56065
#authors    Sekimata, M.; Hiraiwa, M.; Andrien, M.; Dupont, E.; Karaki, S.; Yamamoto, J.; Kano, K.; Takiguchi, M.
#journal     J. Immunol. (1990) 144:3228-3233
#title       Allodeterminants and evolution of a novel HLA-B5 CREG
              antigen, HLA-B SNA.
#cross-references MUID:90217537
#accession   I56065      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues    1-362 #label RES
#cross-references GB:M33573; NID:gi187745; CDS_PID:gi187746
SUMMARY      #length 362 #molecular-weight 40478 #checksum 9585
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qifkntqtdreslnlrnlrgyngseagsht
      |-----|
      99      108
...
1 match found in sequence:
I37135 ; MHC class I HLA-Cw*0803 - human (fragment)
(from "PIR 50")
ENTRY      I37135      #type fragment
TITLE      MHC class I HLA-Cw*0803 - human (fragment)

```

```

ORGANISM #formal_name Homo sapiens #common_name man
DATE 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
ACCESSIONS I37135
REFERENCE I37120
#authors Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#journal Nature (1992) 357:326-329
#title Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession I37135
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-366 #label RES
#cross-references EMBL:Z15144; NID:g28356; CDS_PID:g28357
SUMMARY #length 366 #checksum 5311
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qkykrqgtdrslrnlrgyngseagsh
99
108
|-----|
1 match found in sequence:
I68747 ; MHC class I lymphocyte antigen - human (fragment)
(from "PIR 50")
ENTRY I68747 #type fragment
TITLE MHC class I lymphocyte antigen - human (fragment)
#formal_name Homo sapiens #common_name man
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I68747
REFERENCE I68747
#authors Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and the
evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68747
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-350 #label RES
#cross-references GB:M28204; NID:g576472; CDS_PID:g576473
SUMMARY #length 350 #checksum 636
SEQUENCE
Found using 'seq1' (seq1.key)
...

77 qifktntqtdreslrlrgyngseagsh
87
96
|-----|
1 match found in sequence:
I68748 ; MHC class I lymphocyte antigen - human (fragment)
(from "PIR 50")
ENTRY I68748 #type fragment
TITLE MHC class I lymphocyte antigen - human (fragment)
#formal_name Homo sapiens #common_name man
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I68748
REFERENCE I68748
#authors Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and the
evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68748
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-290 #label RES
#cross-references GB:M28207; NID:g576478; CDS_PID:g576479
SUMMARY #length 290 #checksum 415
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```

E.H.
Immunogenetics (1989) 29:297-307
#journal Allelic variation in HLA-B and HLA-C sequences and the
#title evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68748
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-358 #label RES
#cross-references GB:M28203; NID:g576474; CDS_PID:g576475
SUMMARY #length 358 #checksum 2000
SEQUENCE
Found using 'seq1' (seq1.key)
...

85 qlsktntqtyreslrlrgyngseagsh
95
104
|-----|
1 match found in sequence:
I68750 ; MHC class I lymphocyte antigen - human (fragment)
(from "PIR 50")
ENTRY I68750 #type fragment
TITLE MHC class I lymphocyte antigen - human (fragment)
#formal_name Homo sapiens #common_name man
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I68750
REFERENCE I68750
#authors Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and the
evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68750
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-290 #label RES
#cross-references GB:M28207; NID:g576478; CDS_PID:g576479
SUMMARY #length 290 #checksum 415
SEQUENCE
Found using 'seq1' (seq1.key)
...

13 qnykrqgaqdrslrnlrgyngseagsh
23
32
|-----|
1 match found in sequence:
I56133 ; MHC class I protein - human
(from "PIR 50")
ENTRY I56133 #type complete
TITLE MHC class I protein - human
#formal_name Homo sapiens #common_name man
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56133
REFERENCE I56133
#authors Zemmour, J.; Little, A.M.; Schendel, D.J.; Parham, P.
#journal J. Immunol. (1992) 148:1941-1948
#title The HLA-A,B 'negative' mutant cell line C1R expresses a novel
HLA-B*35 allele, which also has a point mutation in the
translation initiation codon.
#cross-references MUID:92176661

```

```

#accession I56133
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:M81798; NID:g187858; CDS_PID:g187859
SUMMARY #length 362 #molecular-weight 40515 #checksum 9947
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqttyreslnrlrgyngseagsh
108
|-----|
1 match found in sequence:
I62041; MHC HLA-B71 - human (fragment)
(from "PIR 50")
ENTRY I62041 #type complete
TITLE MHC HLA B71 - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I54308
REFERENCE I54308
#authors Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.
#journal Hum. Immunol. (1993) 37:192-194
#title Molecular characterization of HLA-B71 from an African
#cross-references MUID:94064392
#accession I54308
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-350 #label RES
#cross-references GB:L07950; NID:g307236; CDS_PID:g307237
GENETICS
#note gene name HLA-B
SUMMARY #length 350 #checksum 7005
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqttyreslnrlrgyngseagsh
108
|-----|
1 match found in sequence:
I62041; MHC HLA-B cell surface glycoprotein - human
(from "PIR 50")
ENTRY I62041 #type complete
TITLE MHC HLA-B cell surface glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I62041
REFERENCE I38421
#authors Hildebrand, W.H.; Domene, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62041
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:L11603; NID:g493164; CDS_PID:g493165

```

```

#cross-references GB:L11666; NID:g493160; CDS_PID:g493161
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40433 #checksum 9515
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqttyreslnrlrgyngseagsh
108
|-----|
1 match found in sequence:
I62042; MHC HLA-B cell surface glycoprotein - human
(from "PIR 50")
ENTRY I62042 #type complete
TITLE MHC HLA-B cell surface glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I62042
REFERENCE I38421
#authors Hildebrand, W.H.; Domene, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62042
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:L11604; NID:g493162; CDS_PID:g493163
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40449 #checksum 161
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqttyreslnrlrgyngseagsh
108
|-----|
1 match found in sequence:
I62043; MHC HLA-B cell surface glycoprotein - human
(from "PIR 50")
ENTRY I62043 #type complete
TITLE MHC HLA-B cell surface glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I62043
REFERENCE I38421
#authors Hildebrand, W.H.; Domene, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62043
#status preliminary; translated from GB/EMBL/DBDJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:L11603; NID:g493164; CDS_PID:g493165

```

```

GENETICS
#note
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  qisktntqtyreslnrlrgyynqseagsh
    99 108
    |-----|
1 match found in sequence:
I61859 ; MHC HLA-B14 chain - human
(from "PIR 50")
ENTRY      I61859      #type complete
TITLE      MHC HLA-B14 chain - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE   I61859
#authors    Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal     J. Immunol. (1989) 142:3937-3950
#title       Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession   I61859      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues    1-362 #label RES
#cross-references GB:M24040; NID:g187807; CDS_PID:g386898
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  qifkntqtyrenlrialryynqseagsh
    99 108
    |-----|
1 match found in sequence:
I61859 ; MHC HLA-B14 chain - human
(from "PIR 50")
ENTRY      I61859      #type complete
TITLE      MHC HLA-B14 chain - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE   I61859
#authors    Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal     J. Immunol. (1989) 142:3937-3950
#title       Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession   I61859      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues    1-362 #label RES
#cross-references GB:M24040; NID:g187807; CDS_PID:g386898
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```

...
89  qicknttdreslnrlrgyynqseagsh
    99 108
    |-----|
1 match found in sequence:
I61860 ; MHC HLA-B18 chain - human
(from "PIR 50")
ENTRY      I61860      #type complete
TITLE      MHC HLA-B18 chain - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE   I61860
#authors    Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal     J. Immunol. (1989) 142:3937-3950
#title       Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession   I61860      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues    1-362 #label RES
#cross-references GB:M24039; NID:g187809; CDS_PID:g386899
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  qisktntqtyreslnrlrgyynqseagsh
    99 108
    |-----|
1 match found in sequence:
I54463 ; MHC HLA-B38 chain - human (fragment)
(from "PIR 50")
ENTRY      I54463      #type fragment
TITLE      MHC HLA-B38 chain - human (fragment)
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS
REFERENCE   I54463
#authors    Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.;
            Weiss, E.; Schmidt, H.
#journal     Immunogenetics (1989) 30:200-207
#title       Genetic and serological heterogeneity of the supertypic HLA-B
            locus specificities Bw4 and Bw6.
#cross-references MUID:89379286
#accession   I54463      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues    1-274 #label RES
#cross-references GB:M29864; NID:g187674; CDS_PID:g187675
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

65  qickntqtyrenlrialryynqseagsh
    75 84
    |-----|

```

```

-----
1 match found in sequence:
168774 : MHC HLA-B39 chain - human (fragment)
      (from "PIR 50")
ENTRY   I68774      #type fragment
TITLE   MHC HLA-B39 chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE    07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS
REFERENCE
#authors Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.;
          Weiss, E.; Schmidt, H.
#journal Immunogenetics (1989) 30:200-207
#title   Genetic and serological heterogeneity of the supertypic HLA-B
          locus specificities Bw4 and Bw6.
#cross-references MUID:89379286
#accession I68774
#status      preliminary; translated from GB/EMBL/DBBJ
#molecule_type DNA
#residues    1-274 #label RES
#cross-references GB:M29865; NID:gl87676; CDS_PID:gl87677
SUMMARY      #length 274 #checksum 1017
SEQUENCE
Found using 'seq1' (seq1.key)
...

65 qickntqtdreslnrlrgyynqseagsht
   |-----|
   75 84
...

-----
1 match found in sequence:
154314 : MHC HLA-B39N - human
      (from "PIR 50")
ENTRY   I54314      #type complete
TITLE   MHC HLA-B39N - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE
#authors Ogawa, A.; Tokunaga, K.; Nakajima, F.; Kikuchi, A.; Karaki,
          S.; Kashiwase, K.; Ge, J.; Hannestad, K.; Juji, T.;
          Takiguchi, M.
#journal Hum. Immunol. (1994) 41:241-247
#title   Identification of the gene encoding a novel HLA-B39 subtype.
          Two amino acid substitutions on the beta-sheet out of the
          peptide-binding floor form a novel serological epitope.
#cross-references MUID:95189597
#accession I54314
#status      preliminary; translated from GB/EMBL/DBBJ
#molecule_type DNA
#residues    1-362 #label RES
#cross-references GB:L22649; NID:g437369; CDS_PID:g437370
GENETICS
#note       gene name HLA-B
SUMMARY      #length 362 #molecular-weight 40344 #checksum 8904
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qickntqtdreslnrlrgyynqseagsht
   |-----|
   99 108
...

1 match found in sequence:
161864 : MHC HLA-Bw41 chain - human
      (from "PIR 50")
ENTRY   I61864      #type complete
TITLE   MHC HLA-Bw41 chain - human

```

```

-----
1 match found in sequence:
154418 : MHC HLA-B7 heavy chain precursor - human
      (from "PIR 50")
ENTRY   I54418      #type complete
TITLE   MHC HLA-B7 heavy chain precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS
REFERENCE
#authors Sood, A.K.; Pan, J.; Biro, P.A.; Pereira, D.; Srivastava, R.;
          Reddy, V.B.; Ducean, B.W.; Weissman, S.M.
#journal Immunogenetics (1985) 22:101-121
#title   Structure and polymorphism of class I MHC antigen mRNA
          [published erratum appears in Immunogenetics 1986;24
          (4):278].
#cross-references MUID:85287366
#accession I54418
#status      preliminary; translated from GB/EMBL/DBBJ
#molecule_type mRNA
#residues    1-361 #label RES
#cross-references GB:M16102; NID:gl87693; CDS_PID:g307217
SUMMARY      #length 361 #molecular-weight 40366 #checksum 8200
SEQUENCE
Found using 'seq1' (seq1.key)
...

88 qikykaqatdreslnrlrgyynqseagsht
   |-----|
   98 107
...

-----
1 match found in sequence:
184431 : MHC HLA-B8 chain - human
      (from "PIR 50")
ENTRY   I84431      #type complete
TITLE   MHC HLA-B8 chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
          J. Immunol. (1989) 142:3937-3950
#title   Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I84431
#status      preliminary; translated from GB/EMBL/DBBJ
#molecule_type DNA
#residues    1-362 #label RES
#cross-references GB:M24036; NID:gl84169; CDS_PID:g386775
SUMMARY      #length 362 #molecular-weight 40331 #checksum 7954
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifktntqtdreslnrlrgyynqseagsht
   |-----|
   99 108
...

1 match found in sequence:
161864 : MHC HLA-Bw41 chain - human
      (from "PIR 50")
ENTRY   I61864      #type complete
TITLE   MHC HLA-Bw41 chain - human

```

```

ORGANISM      #formal_name Homo sapiens #common_name man
DATE          02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS    I61864
REFERENCE      I36956
#authors       Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal       J. Immunol. (1989) 142:3937-3950
#title         Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession     I61864
##status       preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues     1-362 ##label RES
##cross-references GB:M24033; NID:g187820; CDS_PID:g386903
SUMMARY       #length 362 #molecular-weight 40539 #checksum 9199
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qsktntqtdreslnrgyynqseqsht
          |-----|
          99      108
...
1 match found in sequence:
I61865 ; MHC HLA-B*42 chain - human
(from "PIR 50")
ENTRY     I61865      #type complete
TITLE     MHC HLA-B*42 chain - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSION I61865
REFERENCE  I36956
#authors   Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal   J. Immunol. (1989) 142:3937-3950
#title     Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I61865
##status   preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-362 ##label RES
##cross-references GB:M24034; NID:g187822; CDS_PID:g386904
SUMMARY    #length 362 #molecular-weight 40333 #checksum 8952
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qlykaqatdreslnrgyynqseqsht
          |-----|
          99      108
...
1 match found in sequence:
I61863 ; MHC HLA-B*46 - human
(from "PIR 50")
ENTRY     I61863      #type complete
TITLE     MHC HLA-B*46 - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSION I61863
REFERENCE  I36956
#authors   Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal   J. Immunol. (1989) 142:3937-3950
#title     Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215

```

```

#accession     I61863
##status       preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues     1-362 ##label RES
##cross-references GB:M24033; NID:g187818; CDS_PID:g307227
SUMMARY       #length 362 #molecular-weight 40440 #checksum 9144
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qkykrqatdreslnrgyynqseqsht
          |-----|
          99      108
...
1 match found in sequence:
I61862 ; MHC HLA-B*65 chain - human
(from "PIR 50")
ENTRY     I61862      #type complete
TITLE     MHC HLA-B*65 chain - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS    I61862
REFERENCE      I36956
#authors       Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal       J. Immunol. (1989) 142:3937-3950
#title         Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession     I61862
##status       preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues     1-362 ##label RES
##cross-references GB:M24032; NID:g187816; CDS_PID:g386902
SUMMARY       #length 362 #molecular-weight 40342 #checksum 8952
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qickntqtdreslnrgyynqseqsht
          |-----|
          99      108
...
1 match found in sequence:
I84486 ; transmembrane glycoprotein - human
(from "PIR 50")
ENTRY     I84486      #type complete
TITLE     transmembrane glycoprotein - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS    I84486
REFERENCE      I38421
#authors       Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
                Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
                Bias, W.B.; Parham, P.
#journal       Tissue Antigens (1994) 43:209-218
#title         HLA-B*51: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession     I84486
##status       preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues     1-362 ##label RES
##cross-references GB:L15005; NID:g493154; CDS_PID:g493155
GENETICS
#note          gene name HLA-B*1513

```

```
SUMMARY          #length 362  #molecular-weight 40378  #checksum 9463
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qiskntdtqfyrnlrlalryngqsagshi
    |-----|
    99 108
-----
1 match found in sequence:
155665 ; H-2D cell surface glycoprotein - mouse (fragment)
(from "PIR 50")
ENTRY      I55665      #type fragment
TITLE      H-2D cell surface glycoprotein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
DATE       26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS I55665
REFERENCE   I55665
#authors   Hemmi, S.; Gelliebter, J.; Zeff, R.A.; Melvold, R.W.;
           Nathenson, S.G.
#journal   J. Exp. Med. (1988) 168:2319-2335
#title     Three spontaneous H-2D-b mutants are generated by genetic
           micro-recombination (gene conversion) events: Impact on the
           H-2-restricted immune responsiveness.
#cross-references MUID:89067835
#accession  I55665
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-337 ##label RES
#cross-references GB:M37680; NID:g293733; CDS_PID:g293734
GENETICS
#introns   90/1; 182/1; 274/1; 313/1; 324/1; 337/1
#note      gene name H-2D
#length    337  #checksum 9859
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
64  qkagqeqwfrvsnllgyngqsagsh
    |-----|
    74  83
-----
1 match found in sequence:
170693 ; H-2D cell surface glycoprotein - mouse (fragment)
(from "PIR 50")
ENTRY      I70693      #type fragment
TITLE      H-2D cell surface glycoprotein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I70693
REFERENCE   I55665
#authors   Hemmi, S.; Gelliebter, J.; Zeff, R.A.; Melvold, R.W.;
           Nathenson, S.G.
#journal   J. Exp. Med. (1988) 168:2319-2335
#title     Three spontaneous H-2D-b mutants are generated by genetic
           micro-recombination (gene conversion) events: Impact on the
           H-2-restricted immune responsiveness.
#cross-references MUID:89067835
#accession  I70693
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-337 ##label RES
#cross-references GB:M37681; NID:g293735; CDS_PID:g293736
```

```
GENETICS
#introns   90/1; 182/1; 274/1; 313/1; 324/1; 337/1
#note      gene name H-2D
#length    337  #checksum 9564
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
64  qkagqeqwfrvsnllgyngqsagsh
    |-----|
    74  83
-----
1 match found in sequence:
155961 ; MHC class I H2D-F protein - mouse
(from "PIR 50")
ENTRY      I55961      #type complete
TITLE      MHC class I H2D-P protein - mouse
#formal_name Mus musculus #common_name house mouse
DATE       26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS I55961
REFERENCE   I55961
#authors   Schepart, B.S.; Takahashi, H.; Cozad, K.M.; Murray, R.;
           Ozato, K.; Appella, E.; Frelinger, J.A.
#journal   J. Immunol. (1986) 136:3489-3495
#title     The nucleotide sequence and comparative analysis of the H2D-P
           class I H-2 gene.
#cross-references MUID:86169714
#accession  I55961
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues  1-368 ##label RES
#cross-references GB:M12381; NID:g199418; CDS_PID:g387454
GENETICS
#introns   22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 359/1
#note      gene name H-2D
#length    368  #molecular-weight 41342  #checksum 7387
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
86  qnakdheqsfvsnllgyngqsagsh
    |-----|
    96 105
-----
1 match found in sequence:
157814 ; MHC class I-alpha - mouse
(from "PIR 50")
ENTRY      I57814      #type complete
TITLE      MHC class I-alpha - mouse
#formal_name Mus musculus #common_name house mouse
DATE       02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I57814
REFERENCE   I57814
#authors   Hildebrand, W.H.; Horton, R.M.; Pease, L.R.; Martinko, J.M.
#journal   Mol. Immunol. (1992) 29:61-69
#title     Nucleotide sequence analysis of H-2D(f) and the spontaneous
           in vivo H-2D(fm2) mutation.
#cross-references MUID:92114891
#accession  I57814
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-365 ##label RES
#cross-references GB:M86502; NID:g199306; CDS_PID:g199307
GENETICS
```

```

#note
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qkagqeqwfrvnlrllgynqsgsht
108
|-----|
1 match found in sequence:
I56002 ; MHC H-2D-b protein - mouse
(from "PIR 50")
ENTRY
I56002 #type complete
TITLE
MHC H-2D-b protein - mouse
ORGANISM
#formal_name Mus musculus #common_name house mouse
DATE
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
23-Aug-1996
ACCESSIONS
I56002; I48323
REFERENCE
#authors
Watts, S.; Vogel, J.M.; Harriman, W.D.; Itoh, T.; Stauss,
H.J.; Goodenow, R.S.
#journal
J. Immunol. (1987) 139:3878-3885
#title
DNA sequence analysis of the C3H H-2Kk and H-2Dk loci.
Evolutionary relationships to H-2 genes from four other
mouse strains.
#cross-references MUID:88060499
#accession
I56002
#status
preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues
1-362 #label RES
#cross-references GB:M18523; NID:g199413; CDS_PID:g387452
REFERENCE
I48323
#authors
Joly, E.; Oldstone, M.B.
#journal
Immunogenetics (1991) 34:62-65
#title
Manufacture of a functional cDNA for the H-2Db molecule using
a retroviral shuttle vector.
#cross-references MUID:91310091
#accession
I48323
#status
preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues
1-362 #label RE2
#cross-references EMBL:X52490; NID:g50671; CDS_PID:g50672
GENETICS
#introns
25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 362/1
#note
gene name D(b) gene
#length 362 #molecular-weight 40836 #checksum 8991
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qkagqeqwfrvnlrllgynqsgsht
108
|-----|
1 match found in sequence:
I54531 ; MHC class I protein - rat (fragment)
(from "PIR 50")
ENTRY
I54531 #type fragment
TITLE
MHC class I protein - rat (fragment)
ORGANISM
#formal_name Rattus norvegicus #common_name Norway rat
DATE
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
ACCESSIONS
I54531
REFERENCE
preliminary; translated from GB/EMBL/DBJ
...
#note
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qkagqeqwfrvnlrllgynqsgsht
108
|-----|
1 match found in sequence:
I54554 ; MHC class I RT1.Aw3 protein - rat
(from "PIR 50")
ENTRY
I54554 #type complete
TITLE
MHC class I RT1.Aw3 protein - rat
ORGANISM
#formal_name Rattus norvegicus #common_name Norway rat
DATE
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
ACCESSIONS
I54554
REFERENCE
#authors
Salgar, S.K.; Kunz, H.W.; Gill, T.J.
#journal
Immunogenetics (1995) 42:244-253
#title
Nucleotide sequence and structural analysis of the rat RT1.Eu
and RT1.Aw31 genes, and of genes related to RT1.O and
RT1.C.
#cross-references MUID:95402978
#accession
I54554
#status
preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues
1-360 #label RES
#cross-references GB:L40363; NID:g992566; CDS_PID:g992567
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
79 qkagqeqwfrvnlrllgynqsgsht
98
|-----|
1 match found in sequence:
I68771 ; MHC RT16 protein - rat (fragment)
(from "PIR 50")
ENTRY
I68771 #type fragment
TITLE
MHC RT16 protein - rat (fragment)
ORGANISM
#formal_name Rattus norvegicus #common_name Norway rat
DATE
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
ACCESSIONS
I68771
REFERENCE
#authors
Mauxion, F.; Sobczak, J.; Kress, M.
#journal
Immunogenetics (1989) 29:397-401
#title
Characterization of five distinct cDNA clones encoding for
class I RT1 antigens.
#cross-references MUID:89277428
#accession
I68771
#status
preliminary; translated from GB/EMBL/DBJ

```

```

##molecule_type mRNA
##residues 1-296 #label RES
##cross-references GB:M24023; NID:g2054449; CDS_PID:g205449
SUMMARY #length 296 #checksum 9381
SEQUENCE
Found using 'seq1' (seq1.key)
...

15 qkagneyrvslrnlrgyngseagsh
25 34
|-----|
1 match found in sequence:
S07113 ; class I histocompatibility antigen Ch39 alpha chain -
ENTRY (from "PIR 50")
TITLE class I histocompatibility antigen Ch39 alpha chain -
ORGANISM chimpanzee
#formal_name Pan troglodytes #common_name chimpanzee
DATE 01-Dec-1993 #sequence_revision 01-Dec-1993 #text_change
ACCESSIONS S07113
REFERENCE S06424
#authors Laylor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham,
P.
#journal Nature (1988) 335:268-271
#title HLA-A and B polymorphisms predate the divergence of humans
and chimpanzees.
#cross-references MUID:88319000
#accession S07113
#status preliminary
##residues 1-363 #label LAW
SUMMARY #length 363 #molecular-weight 40540 #checksum 610
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 rnvksaqtdrenlrnlrgyngseagsh
99 108
|-----|
1 match found in sequence:
S06001 ; HLA-B*0703, a B7 variant
ENTRY (from "PIR 50")
TITLE HLA-B*0703 (class I) protein - human
ORGANISM Homo sapiens
#formal_name Homo sapiens #common_name man
DATE 20-Jul-1996 #sequence_revision 20-Jul-1996 #text_change
ACCESSIONS S06001
REFERENCE S06001
#authors Bergmans, A.M.C.; Tijssen, H.; Lardy, N.; Reekers, P.
#journal Hum. Immunol. (1993) 38:159-162
#title Complete nucleotide sequence of HLA-B*0703, a B7 variant
(B*0703).
#accession S06001
#status preliminary
##residues 1-362 #label BER
SUMMARY #length 362 #molecular-weight 40529 #checksum 9704
SEQUENCE
Found using 'seq1' (seq1.key)
...

1 match found in sequence:
S03687 ; Class I histocompatibility antigen H-2DP alpha chain - Mouse
ENTRY (from "PIR 50")
TITLE Class I histocompatibility antigen H-2DP alpha chain - Mouse
(fragment)
ORGANISM Mus musculus #common_name house mouse
DATE 21-Nov-1993 #sequence_revision 21-Nov-1993 #text_change
ACCESSIONS S03687
REFERENCE S03687
#authors Murray, R.; Pederson, K.; Prosser, H.; Muller, D.; Hutchison
III, C.A.; Frelinger, J.A.
#journal Nucleic Acids Res. (1988) 16:9761-9773
#title Random oligonucleotide mutagenesis: application to a large
protein coding sequence of a major histocompatibility
complex class I gene, H-2DP.
#cross-references MUID:89041564
#accession S03687
#status preliminary
##residues 1-90 #label MUR
SUMMARY #length 90 #checksum 1722
SEQUENCE
Found using 'seq1' (seq1.key)
...

65 qnakdheqfrvslrnlrgyngskg
75 84
|-----|
1 match found in sequence:
1A02_PANTR ; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR
ENTRY (from "Swiss-Prot 34")
ID 1A02_PANTR STANDARD; PRT; 362 AA.
AC P16210;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90201944.
RA LAWLOR D.A.; WARREN E.; WARD F.E.; PARHAM P.;
RL IMMUNOL. REV. 113:147-185(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC EMBL; M30679; G176825; -
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
A-5 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
CYTOPLASMIC TAIL.

```

FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40487 MW; 97E6CE8A CRC32;
 Found using 'seq1' (seq1.key)

...

89 qisktnaqtyreslnrlgynyqseagsh
 99 108

...

 1 match found in sequence:
 1A23_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
 (from "Swiss-Prot 34")
 ID 1A23_HUMAN STANDARD; PRT; 365 AA.
 AC P30447;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
 DE PRECURSOR.
 GN HLAA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP MEDLINE: 92104637.
 RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;
 RL IMMUNOGENETICS 35:41-45(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (A*2301).
 RA JORDAN B.R.;
 RL SUBMITTED (XXX-1988) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A. (A*2402/A*2403).
 RX MEDLINE: 92104637.
 RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;
 RL IMMUNOGENETICS 35:41-45(1992).
 RN [4]
 RP SEQUENCE FROM N.A. (A*2402).
 RX MEDLINE: 92269955.
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
 RL NATURE 357:326-329(1992).
 RN [5]
 RP SEQUENCE OF 26-206 FROM N.A.
 RA GAO X., MCCLUSKEY J.;
 RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC -1- POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A*2301 WHICH IS
 SHOWN HERE.
 DR EMBL; M64742; G187618; -.
 DR HSSP; P01892; 1HHG.
 DR MIM; 142800; -.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 ALPHA CHAIN A-23(A9).
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 365 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 365 AA; 40732 MW; B1C21094 CRC32;
 Found using 'seq1' (seq1.key)

...

89 gkvkhsqtdrenlrlgynyqseagsh
 99 108

...

 1 match found in sequence:
 1A24_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN
 (from "Swiss-Prot 34")
 ID 1A24_HUMAN STANDARD; PRT; 365 AA.

AC P05534; P30448; P30449;
 DT 01-NOV-1988 (REL. 09, CREATED)
 DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN
 DE PRECURSOR (AW-24).
 GN HLAA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A. (A*2401).
 RX MEDLINE: 85206128.
 RA N'GUYEN C., SODOYER R., TRUCY J., STRACHAN T., JORDAN B.R.;
 RL IMMUNOGENETICS 21:479-489(1985).
 RN [2]
 RP REVISIONS (A*2401).
 RA JORDAN B.R.;
 RL SUBMITTED (XXX-1988) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A. (A*2402/A*2403).
 RX MEDLINE: 92104637.
 RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;
 RL IMMUNOGENETICS 35:41-45(1992).
 RN [4]
 RP SEQUENCE FROM N.A. (A*2402).
 RX MEDLINE: 92269955.
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
 RL NATURE 357:326-329(1992).
 RN [5]
 RP SEQUENCE OF 26-206 FROM N.A.
 RA GAO X., MCCLUSKEY J.;
 RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC -1- POLYMORPHISM: THE FOLLOWING ALLELES OF A-24 ARE KNOWN: A*2401,
 A*2401 AND A*2403. THE SEQUENCE SHOWN IS THAT OF A*2401.
 DR EMBL; M15497; G386877; -.
 DR EMBL; M64740; G187614; -.
 DR EMBL; M64741; G187616; -.
 DR EMBL; U19733; G624267; -.
 DR EMBL; U18987; G624267; JOINED.
 DR HSSP; P01892; 1HHG.
 DR MIM; 142800; -.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; POLYMORPHISM.
 FT SIGNAL 1 24
 FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 ALPHA CHAIN A-24(A9).
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 308 CONNECTING PEPTIDE.
 FT TRANSMEM 309 332
 FT DOMAIN 333 365 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT VARIANT 5 5 G -> A (IN A*2402 AND A*2403).
 FT VARIANT 180 180 Q -> W (IN REF. 5).
 FT VARIANT 190 191 DG -> EW (IN A*2403).
 FT VARIANT 206 206 A -> T (IN A*2402, A*2403 AND REF. 5).
 SQ SEQUENCE 365 AA; 40644 MW; DE23D06E CRC32;
 Found using 'seq1' (seq1.key)

...

89 gkvkhsqtdrenlrlgynyqseagsh
 99 108

```

...
-----
1 match found in sequence:
1A25_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A25_HUMAN STANDARD; PRT; 365 AA.
AC P18462;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
DE PRECURSOR.
DE HLA.
GN HLA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A. (A*2501).
RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-25 KNOWN IS A*2501 WHICH IS
CC SHOWN HERE.
DR EMBL; M32321; G307225; -.
DR PIR; A35997; A35997.
DR HSP; P01891; 1HSB.
DR MIM; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 1 25 365
FT FT
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-25(A-10).
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41218 MW; 131A8F20 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
99 108
...
-----
1 match found in sequence:
1A32_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A32_HUMAN STANDARD; PRT; 365 AA.
AC P10314;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
DE PRECURSOR.
DE HLA.
GN HLA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A. (A*2501).
RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-25 KNOWN IS A*2501 WHICH IS
CC SHOWN HERE.
DR EMBL; M32321; G307225; -.
DR PIR; A35997; A35997.
DR HSP; P01891; 1HSB.
DR MIM; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 1 25 365
FT FT
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-25(A-10).
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41218 MW; 131A8F20 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
99 108
...
-----
1 match found in sequence:
1A25_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A25_HUMAN STANDARD; PRT; 365 AA.
AC P18462;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
DE PRECURSOR.
DE HLA.
GN HLA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A. (A*2501).
RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-25 KNOWN IS A*2501 WHICH IS
CC SHOWN HERE.
DR EMBL; M32321; G307225; -.
DR PIR; A35997; A35997.
DR HSP; P01891; 1HSB.
DR MIM; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 1 25 365
FT FT
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-25(A-10).
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41218 MW; 131A8F20 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
99 108
...
-----
1 match found in sequence:
1A32_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A32_HUMAN STANDARD; PRT; 365 AA.
AC P10314;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
DE PRECURSOR.
DE HLA.
GN HLA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A. (A*2501).
RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-25 KNOWN IS A*2501 WHICH IS
CC SHOWN HERE.
DR EMBL; M32321; G307225; -.
DR PIR; A35997; A35997.
DR HSP; P01891; 1HSB.
DR MIM; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 1 25 365
FT FT
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-32(AW-19).
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41218 MW; 131A8F20 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
99 108
...
-----
1 match found in sequence:
1B01_GORGO ; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
ID 1B01_GORGO STANDARD; PRT; 362 AA.
AC P30379;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
DE GORILLA GORILLA (LOWLAND GORILLA).
DE OS
DE EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
DE EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; X60255; G22866; -.
DR PIR; J05339; J05339.
DR HSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 1 25 362
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,

```

```

RN [1]
RP SEQUENCE FROM N.A. (A*3201).
RA DOMENA J.D.;
RL SUBMITTED (DEC-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 25-298 FROM N.A. (A*3201).
RX MEDLINE; 87058961.
RA WAN A.M., ENNIS P., PARHAM P., HOLMES N.;
J. IMMUNOL. 137:3671-3674(1986)
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-32 KNOWN IS A*3201 WHICH IS
CC SHOWN HERE.
DR EMBL; U03907; G432996; -.
DR PIR; A26088; HLH032.
DR HSP; P01892; 1HHG.
DR MIM; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 1 25 365
FT FT
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-32(AW-19).
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT TRANSMEM 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41048 MW; 71FA7IA9 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
99 108
...
-----
1 match found in sequence:
1B01_GORGO ; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
ID 1B01_GORGO STANDARD; PRT; 362 AA.
AC P30379;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
DE GORILLA GORILLA (LOWLAND GORILLA).
DE OS
DE EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
DE EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; X60255; G22866; -.
DR PIR; J05339; J05339.
DR HSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 1 25 362
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,

```

```

FT DOMAIN 25 114 GOGO-B0101 ALPHA CHAIN.
FT DOMAIN 113 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;
Found using 'seq1' (seq1.key)
...

```

```

89 qtskaqactdrenlrialryynqseagsh
99 108
|-----|

```

```

1 match found in sequence:
1B01_PANTR ; CHIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")

```

```

ID 1B01_PANTR STANDARD; PRT; 359 AA.
AC P13750;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CHIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
DE (FRAGMENT).
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89030641.
RA MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
RA KLEIN J.;
RL EMBO J. 7:2765-2774(1988).
RN [2]
RP REVISIONS.
RA NAYER W.;
RL SUBMITTED (FEB-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; X13115; G755776; -.
DR PIR; S03537; S03537.
DR HSSP; P03989; IHSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 20
FT CHAIN 21 359

```

```

CHIA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-1 ALPHA CHAIN.
FT DOMAIN 21 110
FT DOMAIN 111 202 EXTRACELLULAR ALPHA-1.
FT DOMAIN 203 294 EXTRACELLULAR ALPHA-2.
FT DOMAIN 295 305 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 306 329 CONNECTING PEPTIDE.
FT DOMAIN 330 359
FT DISULFID 121 184 CYTOPLASMIC TAIL.
FT DISULFID 223 279 BY SIMILARITY.
FT CARBOHYD 106 106 BY SIMILARITY.
SQ SEQUENCE 359 AA; 40173 MW; 5395FFC9 CRC32;
Found using 'seq1' (seq1.key)
...

```

```

|-----|

```

```

85 rmkasaqtdrenlrialryynqseagsh
99 104

```

```

1 match found in sequence:

```

```

1B02_GORG0 ; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
ID 1B02_GORG0 STANDARD; PRT; 362 AA.
AC P30380;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLER D.A., WARREN E., TAYLOR P., FARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; X60693; G22868; -.
DR PIR; JH0540; JH0540.
DR HSSP; P03989; IHSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 BY SIMILARITY.
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-B0102 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 299 308 CONNECTING PEPTIDE.
FT DOMAIN 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40204 MW; 3CF119AD CRC32;
Found using 'seq1' (seq1.key)
...

```

```

89 qtskaqactdrenlrialryynqseagsh
99 108
|-----|

```

```

1 match found in sequence:
1B02_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B02_HUMAN STANDARD; PRT; 362 AA.
AC P01889;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
DE PRECURSOR (B7.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.

```

```

RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90315860.
RA PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D.,
RA KRENSKY A.M., LAWLER D.A., LITTMAN D.R., NORMENT A.M., ORR H.T.,
RA SALTER R.D., ZEMMOUR J.;
RL COLD SPRING HARB. SYMP. QUANT. BIOL. 54:529-543(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85287366.
RA SOOD A.K., PAN J., BIRO P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
RA DUCEMAN B.W., WEISSMAN S.M.;
RL IMMUNOGENETICS 22:101-121(1985).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 80088278.
RA ORR H.T., LOPEZ DE CASTRO J.A., LANCET D., STROMINGER J.L.;
RL BIOCHEMISTRY 18:5711-5720(1979).
RN [5]
RP SEQUENCE OF 25-295.
RA ELLEXSON M.E., ZHANG L., HILDBRAND W.H.;
RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [5]
RP SEQUENCE OF 25-295.
RX MEDLINE; 80088278.
RA ORR H.T., LOPEZ DE CASTRO J.A., LANCET D., STROMINGER J.L.;
RL BIOCHEMISTRY 18:5711-5720(1979).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M32317; G307221; -.
DR EMBL; M16102; G307217; ALT_SEQ.
DR EMBL; U29057; G1213467; -.
DR PIR; A02185; HLHUB7.
DR PIR; B35997; B35997.
DR HSSP; P03989; IHSB.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CONFLICT 15 18
FT CONFLICT 266 266
FT CONFLICT 268 268
FT CONFLICT 297 297
FT CONFLICT 314 315
SQ SEQUENCE 362 AA; 40460 MW; 87B2ED84 CRC32;
Found using 'seq1' (seq1.key)
...
89 qlykaqaqtreslnlrgyynqseagsh
|-----|
99 108
...
1 match found in sequence:
1B02_PANTR; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")
ID 1B02_PANTR STANDARD; PRT; 362 AA.
AC P13751;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)

```

```

DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89030641.
RA MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
RA KLEIN J.;
RL EMBO J. 7:2765-2774(1988).
RN [2]
RP REVISIONS.
RA MAYER W.;
RL SUBMITTED (FEB-1989) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X13116; G38209; -.
DR PIR; S03538; S03538.
DR HSSP; P03989; IHSB.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 362 AA; 40488 MW; 4BF65A6C CRC32;
Found using 'seq1' (seq1.key)
...
89 qisktnaqtreslnlrgyynqseagshi
|-----|
99 108
...
1 match found in sequence:
1B03_GORGO; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
ID 1B03_GORGO STANDARD; PRT; 362 AA.
AC P30381;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X60254; G22870; -.
DR PIR; JH0541; JH0541.
DR HSSP; P03989; IHSB.
DR PROSITE; PS00290; IG_MHC.

```

```

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT GOGO-B0103 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40248 MW; FEA6A941 CRC32;
Found using 'seq1' (seq1.key)

...

89 qtskacqatdrenlrtrialryynqseqsht
99 108
|-----|
1 match found in sequence:
1B04_HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B04_HUMAN STANDARD; PRT; 362 AA.
AC P30460;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P.; LAWLER D.A.; LOMEN C.E.; ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC EMBL; M24036; G386775; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-8 B*0801.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40331 MW; 1467B8EB CRC32;
Found using 'seq1' (seq1.key)

...

```

```

89 qifkntqtdreslnrlrgyynqseqsht
99 108
|-----|

```

```

...

1 match found in sequence:
1B07_HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B07_HUMAN STANDARD; PRT; 362 AA.
AC P30462;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P.; LAWLER D.A.; LOMEN C.E.; ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC EMBL; M24040; G386898; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-14 B*1401.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40358 MW; 9BED8199 CRC32;
Found using 'seq1' (seq1.key)

...

89 qickntqtdreslnrlrgyynqseqsht
99 108
|-----|
1 match found in sequence:
1B08_HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA
(from "Swiss-Prot 34")
ID 1B08_HUMAN STANDARD; PRT; 362 AA.
AC P30463;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.

```

```

RA PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24032; G386902; -.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT DOMAIN 310 333
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40342 MW; BE68AC9E CRC32;
Found using 'seq1' (seq1.key)

...

89 qickntntqtdreslnrlrgyngsagsh
108
-----|
1 match found in sequence:
1B10_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA
(from "Swiss-Prot 34")
ID 1B10_HUMAN STANDARD; PRT; 362 AA.
AC P30464;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92196792.
RA LITTLE A.-M., PARHAM P.;
RA TISSUE ANTIGENS 38:186-190(1991).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M75138; G187710; -.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT CARBOHYD 110 110
BY SIMILARITY.

```

```

FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40338 MW; 8CF9BCD0 CRC32;
Found using 'seq1' (seq1.key)

...

89 qickntntqtdreslnrlrgyngsagshi
108
-----|
1 match found in sequence:
1B11_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
(from "Swiss-Prot 34")
ID 1B11_HUMAN STANDARD; PRT; 362 AA.
AC P30465;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTEL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X61709; G32189; -.
DR PIR; S16789; S16789.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40387 MW; 99D70546 CRC32;
Found using 'seq1' (seq1.key)

...

89 qickntntqtdreslnrlrgyngsagsh
108
-----|
1 match found in sequence:
1B12_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B12_HUMAN STANDARD; PRT; 362 AA.

```

```

AC P30513;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE: 92269956.
RA WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
RA LEVINE C.G., GABER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
RA TROOP G.M., HUGHES A.L., LETVIN N.L.;
RL NATURE 357:329-333(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84382; G187714; -.
DR PIR; S24433; S24433.
DR HSSP; P03989; IHSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-62 B*1504.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40406 MW; E80FC24C CRC32;
Found using 'seq1' (seq1.key)
...

89 qiskntqtyreslnrlgynyqseqsht
99 108
...

1 match found in sequence:
1B15_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B15_HUMAN STANDARD; PRT; 362 AA.
AC P10317;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
DE PRECURSOR (B-27K) (B27.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 86220133.
RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
RL EMBO J. 5:547-552(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA PARHAM P., ARNETT K.L., ADAMS E.J.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE OF 86-107 AND 171-181.
RX MEDLINE; 86042671.
RA VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
RA LOPEZ DE CASTRO J.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 82:7394-7398(1985).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X03664; G871296; -.
DR EMBL; X03667; G871296; JOINED.
DR EMBL; L38504; G896271; -.
DR PIR; B25092; HLHUBK.
DR HSSP; P03989; IHSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-27 B*2702 ALPHA CHAIN
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40406 MW; E80FC24C CRC32;
Found using 'seq1' (seq1.key)
...

89 qiskntqtyreslnrlgynyqseqsht
99 108
...

1 match found in sequence:
1B13_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B13_HUMAN STANDARD; PRT; 362 AA.
AC P30466;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

```

```

89      qlfktntqtyreslnrgyynqseagshi
      99      108
      |-----|
      1 match found in sequence:
      1B22_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
      (from "Swiss-Prot 34")
      ID 1B22_HUMAN STANDARD; PRT; 362 AA.
      AC P30468;
      DT 01-APR-1993 (REL. 25, CREATED)
      DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
      DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
      DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
      DE DE PRECURSOR.
      GN HLAB.
      OS HOMO SAPIENS (HUMAN).
      OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
      OC EUTHERIA; PRIMATES.
      RN [1]
      RP SEQUENCE FROM N.A.
      RX MEDLINE; 91365651.
      RA CHERTKOFF L.P., HERRERA M., FAINBOIM L., SATZ M.L.;
      RL HUM. IMMUNOL. 31:153-158(1991).
      CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
      CC THE IMMUNE SYSTEM.
      CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
      CC MICROGLOBULIN).
      DR EMBL; M63454; G403145; -.
      DR HSPF; P03989; IHS4.
      DR MIN; 142830; -.
      DR PROSITE; PS00290; IG_MHC.
      KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
      FT SIGNAL 1 24
      FT CHAIN 25 362
      FT DOMAIN 25 114
      FT DOMAIN 115 206
      FT DOMAIN 207 298
      FT DOMAIN 299 308
      FT TRANSMEM 309 332
      FT DOMAIN 333 362
      FT CARBOHYD 110 110
      FT DISULFID 125 188
      FT DISULFID 227 283
      SQ SEQUENCE 362 AA; 40564 MW; D7B5C2C9 CRC32;
      Found using 'seq1' (seq1.key)
      ...
      |-----|
      89      qlfktntqtyreslnrgyynqseagshi
      99      108
      1 match found in sequence:
      1B23_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
      (from "Swiss-Prot 34")
      ID 1B23_HUMAN STANDARD; PRT; 362 AA.
      AC P30469;
      DT 01-APR-1993 (REL. 25, CREATED)
      DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
      DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
      DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
      DE DE PRECURSOR.
      GN HLAB.
      OS HOMO SAPIENS (HUMAN).
      OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

```

```

OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92176661.
RA ZEMMOUR J., LITTLE A.M., SCHENDEL D.J., PARHAM P.;
RL J. IMMUNOL. 148:1194-1948(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M81798; G187859; -.
DR HSP; P03989; IHSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-35 B*3503.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40515 MW; 4222D30A CRC32;
Found using 'seq1' (seq1.key)
...

89 gikfntqtqyreslnrlrgyynqseagshi
99 108
...

1 match found in sequence:
1B24_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B24_HUMAN STANDARD; PRT; 354 AA.
AC P30470;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN
DE PRECURSOR (FRAGMENT).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92269956.
RA WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
RA LEVINE C.G., GABER T.L., DOON A.L., LORD C.I., GHIM S.H.,
RA TROUP G.M., HUGHES A.L., LETVIN N.L.;
RL NATURE 357:329-333(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M86403; -. NOT_ANNOTATED_CDS.
DR HSP; P03989; IHSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 354 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-35 B*3504.

```

```

FT DOMAIN 17 106 EXTRACELLULAR ALPHA-1.
FT DOMAIN 107 198 EXTRACELLULAR ALPHA-2.
FT DOMAIN 199 290 EXTRACELLULAR ALPHA-3.
FT DOMAIN 291 300 CONNECTING PEPTIDE.
FT TRANSEM 301 324
FT DOMAIN 325 354 CYTOPLASMIC TAIL.
FT CARBOHYD 102 102 BY SIMILARITY.
FT DISULFID 117 180 BY SIMILARITY.
FT DISULFID 219 275 BY SIMILARITY.
SQ SEQUENCE 354 AA; 39617 MW; 6564795A CRC32;
Found using 'seq1' (seq1.key)
...

81 gikfntqtqyreslnrlrgyynqseagshi
91 100
...

1 match found in sequence:
1B25_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3505 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B25_HUMAN STANDARD; PRT; 362 AA.
AC P30471;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3505 ALPHA CHAIN
DE PRECURSOR (B35-G).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-328(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84385; G187720; -.
DR HSP; P03989; IHSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-35 B*3505.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40374 MW; B404A7FA CRC32;
Found using 'seq1' (seq1.key)
...

89 gikfntqtqyreslnrlrgyynqseagsh
99 108
...

```

```

CC  -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC  THE IMMUNE SYSTEM.
CC  -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC  MICROGLOBULIN).
DR  EMBL; L04695; G187893; -.
DR  HSSP; P03989; IHSA.
DR  MIM; 142830; -.
DR  PROSITE; PS00290; IG_MHC.
KW  MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT  SIGNAL 1 24
FT  CHAIN 25 362
FT
FT  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT  ALPHA CHAIN B-35 B*3507.
FT  DOMAIN 25 114
FT  DOMAIN 115 206
FT  DOMAIN 207 298
FT  DOMAIN 299 308
FT  TRANSMEM 309 332
FT  DOMAIN 333 362
FT  CARBOHYD 110 110
FT  DISULFID 125 188
FT  DISULFID 227 283
SQ  SEQUENCE 362 AA; 40497 MW; 9F979909 CRC32;
Found using 'seq1' (seq1.key)
...
89 qifkntqtqvieslrnlrgvynqseagshi
|-----|
99 108
...
1 match found in sequence:
1B28_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3508 ALPHA CHAIN
(from 'Swiss-Prot 34')
ID 1B28_HUMAN STANDARD; PRT; 362 AA.
AC P30474;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3508 ALPHA CHAIN
DE PRECURSOR.
DE GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 93303752.
RA THEILER G., PANDO M., DELFINO J.M., TAKIGUCHI M., SATZ M.L.;
RL TISSUE ANTIGENS 41:143-147(1993).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE; 94186367.
RA STEINLE A., REINHARDT C., NOESSNER E., UCHANSKA-ZIEGLER B.,
RA ZIEGLER A., SCHENDEL D.J.;
RL HUM. IMMUNOL. 38:261-269(1993).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR  EMBL; L04696; G184216; -.
DR  EMBL; Z22651; G297143; -.
DR  PIR; S32754; S32754.
DR  PIR; S32755; S32755.
DR  HSSP; P03989; IHSA.
DR  MIM; 142830; -.
DR  PROSITE; PS00290; IG_MHC.
KW  MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT  SIGNAL 1 24
FT  CHAIN 25 362
FT
FT  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT  ALPHA CHAIN B-35 B*3508.

```



```

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE.
RX MEDLINE: 8400412.
RA LOPEZ DE CASTRO J.A., BRAGADO R., STRONG D.M., STROMINGER J.L.;
RL BIOCHEMISTRY 22:3961-3969(1983).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
    THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
    MICROGLOBULIN).
CC PIR: A02186; HLH040.
DR HSSP: P03989; 1HSA.
DR MIM: 142830.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; GLYCOPROTEIN.
FT DOMAIN 1 90 EXTRACELLULAR ALPHA-1.
FT DOMAIN 91 181 EXTRACELLULAR ALPHA-2.
FT DOMAIN 182 >270 EXTRACELLULAR ALPHA-3.
FT CARBOHYD 86 86
FT DISULFID 101 153
FT DISULFID 202 258
FT NON_TER 270 270
SQ SEQUENCE 270 AA; 31205 MW; BFE44EFF CRC32;
Found using 'seq1' (seq1.key)
...

```

```

65 qiskntqttyreslnlrgyynqseqsgh
75
84

```

```

-----
1 match found in sequence:
1B34_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B34_HUMAN STANDARD; PRT; 362 AA.
AC Q04826;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93127148.
RA DOMENA J.D., JOHNSTON-DOW L., PARHAM P.;
RL TISSUE ANTIGENS 40:254-256(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
    THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
    MICROGLOBULIN).
CC EMBL: L09736; G187679; -.
DR HSSP: P03989; 1HSA.
DR MIM: 142830.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
    ALPHA CHAIN B-40 B*4002.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT CARBOHYD 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40600 MW; EIFE537C CRC32;
Found using 'seq1' (seq1.key)
...

```

```

FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40505 MW; C2A00916 CRC32;
Found using 'seq1' (seq1.key)
...

```

```

89 qiskntqttyreslnlrgyynqseqsgh
99
108

```

```

-----
1 match found in sequence:
1B35_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4003 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B35_HUMAN STANDARD; PRT; 362 AA.
AC P30477;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4003 ALPHA CHAIN
DE PRECURSOR (B40-G1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
    THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
    MICROGLOBULIN).
CC EMBL: M84384; G187718; -.
DR HSSP: P03989; 1HSA.
DR MIM: 142830.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
    ALPHA CHAIN B-40 B*4003.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT CARBOHYD 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40600 MW; EIFE537C CRC32;
Found using 'seq1' (seq1.key)
...

```

```

89 qiskntqttyreslnlrgyynqseqsgh
99
108

```

```

-----
1 match found in sequence:
1B36_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4004 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B36_HUMAN STANDARD; PRT; 362 AA.
AC P30478;

```

```

DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4004 ALPHA CHAIN
DE PRECURSOR (B40-G2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92269955.
RA BELMICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84383; G187716; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-40 B*4004 ALPHA CHAIN
FT DOMAIN 25 114 ALPHA CHAIN B-40 B*4004.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40430 MW; 3797AB68 CRC32;
Found using 'seq1' (seq1.key)
...

89 qiskntqtyreslnrgynqseagst
|-----|
99 108
1 match found in sequence:
1B38_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-41 B*4101 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B38_HUMAN STANDARD; PRT; 362 AA.
AC P30479;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-41 B*4101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24034; G386904; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT BW-41 B*4101 ALPHA CHAIN
FT DOMAIN 25 114 ALPHA CHAIN BW-41 B*4101.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 310 333 CONNECTING PEPTIDE.
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40333 MW; 795A36FD CRC32;
Found using 'seq1' (seq1.key)
...

```

```

DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-41 B*4101.
FT DOMAIN 25 114 ALPHA CHAIN B-41 B*4101.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 310 333 CONNECTING PEPTIDE.
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40539 MW; A292D60A CRC32;
Found using 'seq1' (seq1.key)
...

89 qiskntqtyreslnrgynqseagst
|-----|
99 108
1 match found in sequence:
1B39_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-42 B*4201 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B39_HUMAN STANDARD; PRT; 362 AA.
AC P30480;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-42 B*4201 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24034; G386904; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT BW-42 B*4201.
FT DOMAIN 25 114 ALPHA CHAIN BW-42 B*4201.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 310 333 CONNECTING PEPTIDE.
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40333 MW; 795A36FD CRC32;
Found using 'seq1' (seq1.key)
...

```

|-----|

89 qiykaqatdreslnlrgyynqseagsh
99 108

...

1 match found in sequence:
1B43_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-45(B-12) B*4501 ALPHA
(from "Swiss-Prot 34")
ID 1B43_HUMAN STANDARD; PRT; 362 AA.
AC P30483;
DT 01-APR-1993 (REL. 25, CREATED)
DI 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-45(B-12) B*4501 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; X61710; G32183; -.
DR PIR; S16772; S16772.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN BW-45 B*4501.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40414 MW; 989A5539 CRC32;
Found using 'seq1' (seq1.key)

...

89 giskntqtdreslnlrgyynqseagsh
99 108

...

1 match found in sequence:
1B44_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-46 B*4601 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B44_HUMAN STANDARD; PRT; 362 AA.
AC P30484;
DT 01-APR-1993 (REL. 25, CREATED)
DI 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-46 B*4601 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; M84380; G187708; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B*4601.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40414 MW; 989A5539 CRC32;
Found using 'seq1' (seq1.key)

...

89 giskntqtdreslnlrgyynqseagsh
99 108

...

1 match found in sequence:
1B46_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B46_HUMAN STANDARD; PRT; 362 AA.
AC P30486;
DT 01-APR-1993 (REL. 25, CREATED)
DI 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; M84380; G187708; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-48 B*4801.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40440 MW; EC587DD3 CRC32;
Found using 'seq1' (seq1.key)

...

89 qkykrqatdreslnlrgyynqseagsh
99 108

...

1 match found in sequence:
1B46_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B46_HUMAN STANDARD; PRT; 362 AA.
AC P30486;
DT 01-APR-1993 (REL. 25, CREATED)
DI 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; M84380; G187708; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-48 B*4801.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40440 MW; EC587DD3 CRC32;
Found using 'seq1' (seq1.key)

[illegible]

```

FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40362 MW; 081D8291 CRC32;
Found using 'seq1' (seq1.key)

...

89 gskstntqyreslnrlgyynqseagsh
99
108
}-----|
1 match found in sequence:
1B47_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA C
(from "Swiss-Prot 34")
ID 1B47_HUMAN STANDARD; PRT; 362 AA.
AC P30487;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056529.
RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
RA WILLIAMS R.C., PARHAM P.;
RL J. IMMUNOL. 149:3563-3568(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24037; G407191; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-49(B-21) B*4901.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 299 309 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 310 333 CONNECTING PEPTIDE.
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;
Found using 'seq1' (seq1.key)

...

89 gskstntqyrenrlalryynqseagsh
99
108
}-----|
1 match found in sequence:
1B49_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CH
(from "Swiss-Prot 34")
ID 1B49_HUMAN STANDARD; PRT; 362 AA.
AC P18464;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

```

```

...

99 108
}-----|
1 match found in sequence:
1B48_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-50(B-21) B*5001 ALPHA
(from "Swiss-Prot 34")
ID 1B48_HUMAN STANDARD; PRT; 362 AA.
AC P30488;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-50(B-21) B*5001 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X61706; G32185; -.
DR PIR; S16773; S16773.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN BW-50(B-21) B*5001.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 299 309 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 310 333 CONNECTING PEPTIDE.
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40541 MW; 6C8B4A34 CRC32;
Found using 'seq1' (seq1.key)

...

89 gskstntqyreslnrlgyynqseagsh
99
108
}-----|
1 match found in sequence:
1B49_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CH
(from "Swiss-Prot 34")
ID 1B49_HUMAN STANDARD; PRT; 362 AA.
AC P18464;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

```

```

OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RL TAKIGUCHI M.;
RN J. IMMUNOL. 142:306-311(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89233295.
RA POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
RL IMMUNOGENETICS 29:297-307(1989).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M32319; G307223;
DR EMBL; M22792; G553533; ALT_SEQ.
DR EMBL; M22786; G553533; JOINED.
DR EMBL; M22787; G553533; JOINED.
DR EMBL; M22788; G553533; JOINED.
DR EMBL; M22789; G553533; JOINED.
DR EMBL; M22790; G553533; JOINED.
DR EMBL; M22791; G553533; JOINED.
DR EMBL; L41087; G735902;
DR EMBL; L41086; G735902; JOINED.
DR PIR; A30345; A30345.
DR PIR; A30548; A30548.
DR HSSP; P03989; ILSA.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-51(B-5) B*5104.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;
Found using 'seq1' (seq1.key)
...

89 qifkntqtyrenlrialryngseagshi
|-----|
99 108

1 match found in sequence:
1B52_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CH
(from "Swiss-Prot 34")
ID 1B52_HUMAN STANDARD; PRT; 362 AA.
AC P30489;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RN J. IMMUNOL. 142:306-311(1989).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M22799; G553538; ALT_SEQ.
DR EMBL; M22793; G553538; JOINED.
DR EMBL; M22794; G553538; JOINED.
DR EMBL; M22795; G553538; JOINED.
DR EMBL; M22796; G553538; JOINED.
DR EMBL; M22797; G553538; JOINED.
DR EMBL; M22798; G553538; JOINED.
DR PIR; B30345; B30345.
...

89 qifkntqtyrenlrialryngseagsh
|-----|
99 108

1 match found in sequence:
1B53_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA C
(from "Swiss-Prot 34")
ID 1B53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RN J. IMMUNOL. 142:306-311(1989).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M22799; G553538; ALT_SEQ.
DR EMBL; M22793; G553538; JOINED.
DR EMBL; M22794; G553538; JOINED.
DR EMBL; M22795; G553538; JOINED.
DR EMBL; M22796; G553538; JOINED.
DR EMBL; M22797; G553538; JOINED.
DR EMBL; M22798; G553538; JOINED.
DR PIR; B30345; B30345.
...

```

```

DR PIR: B30548; B30548.
DR HSP: P03989; ILSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40521 MW; 3B436FE8 CRC32;
Found using 'seq1' (seq1.key)
...

89 qlskntqttyrenlrialryynqseagsh
99 108
-----|
1 match found in sequence:
1B54_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B54_HUMAN STANDARD; PRT; 362 AA.
AC P30491.
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91033941.
RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,
RA TAKIGUCHI M.;
RL IMMUNOGENETICS 32:195-199(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL: M58636; G187757; -.
DR EMBL; M58636; G187757; -.
DR HSP: P03989; ILSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;
Found using 'seq1' (seq1.key)
...

1 match found in sequence:
1B54_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B54_HUMAN STANDARD; PRT; 362 AA.
AC P30491.
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91033941.
RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,
RA TAKIGUCHI M.;
RL IMMUNOGENETICS 32:195-199(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL: M58636; G187757; -.
DR EMBL; M58636; G187757; -.
DR PIR: A45834; A45834.
DR HSP: P03989; ILSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;
Found using 'seq1' (seq1.key)
...

```

```

...
89 qifkntqttyrenlrialryynqseagsh
99 108
-----|
1 match found in sequence:
1B55_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-54 (BW-22) B*5401 ALPHA
(from "Swiss-Prot 34")
ID 1B55_HUMAN STANDARD; PRT; 362 AA.
AC P30492.
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-54 (BW-22) B*5401 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92148136.
RA HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
RL J. IMMUNOL. 148:1155-1162(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL: M7774; G184117; -.
DR EMBL; M7774; G184117; -.
DR HSP: P03989; ILSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40380 MW; A34A10EC CRC32;
Found using 'seq1' (seq1.key)
...

89 qiykaqaqtdreslnrlrgyynqseagsh
99 108
-----|
1 match found in sequence:
1B56_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55 (BW-22) B*5501 ALPHA
(from "Swiss-Prot 34")
ID 1B56_HUMAN STANDARD; PRT; 362 AA.
AC P30493.
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55 (BW-22) B*5501 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.

```



```

1B59_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5602 ALPHA
(from "Swiss-Prot 34")
ID 1B59_HUMAN STANDARD; PRT; 362 AA.
AC P30456;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5602 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92148136.
RA HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
RL J. IMMUNOL. 148:1155-1162(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL: M7775; G184125; -.
DR HSSP: P03989; 1HSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN BW-56(BW-22) B*5602.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40460 MW; 64608CFE CRC32;
found using 'seq1' (seq1.key)
...
89 qiykaqatdreslnrlryynqseagsht
99 108
[1]
1 match found in sequence:
1B60_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
(from "Swiss-Prot 34")
ID 1B60_HUMAN STANDARD; PRT; 362 AA.
AC P18465;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
DE CHAIN PRECURSOR (BW57.1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91067476.

```

```

RA ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
RL NUCLEIC ACIDS RES. 18:6702-6702(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL: M32318; G307222; -.
DR EMBL: X55711; G32181; -.
DR PIR: S12622; S12622.
DR PIR: D35997; D35997.
DR HSSP: P03989; 1HSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-57(B-17) B*5701.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40224 MW; D91DF8DD CRC32;
found using 'seq1' (seq1.key)
...
89 rnmkasaqtyrenlnrlryynqseagshi
99 108
[1]
1 match found in sequence:
1B61_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA C
(from "Swiss-Prot 34")
ID 1B61_HUMAN STANDARD; PRT; 362 AA.
AC P30497;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
DE PRECURSOR (BW57.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL: X61707; G32187; -.
DR PIR: S16774; S16774.
DR HSSP: P03989; 1HSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-57(B-17) B*5702.

```



```

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 89215297.
RA ELLIS S.A., STRACHAN T., PALMER M.S., MCMICHAEL A.J.;
RL J. IMMUNOL. 142:3281-3285(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M26429; G307239; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-1 CW*0101.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT CONNECTING PEPTIDE.
FT DOMAIN 334 366
FT CYTOPLASMIC TAIL.
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
FT CARBOHYD 110 110
FT BY SIMILARITY.
SQ SEQUENCE 366 AA; 40964 MW; 922CF5E4 CRC32;
Found using 'seq1' (seq1.key)
...
89 qkynrqatdvrslnrlrgyynqseagst
99 108
...
1 match found in sequence:
1C01.PANTR; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C ALPHA CHAIN PRECURSOR.
(from "Swiss-Prot 34")
ID 1C01.PANTR STANDARD; PRT; 366 AA.
AC P30686;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C ALPHA CHAIN PRECURSOR.
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 92391104.
RA KATO T., ESUMI M., YAMASHITA S., ABE K., SHIKATA T.;
RL VIROLOGY 190:856-860(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; D11383; E56339; ALT_INIT.
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT C ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.

```

```

FT TRANSMEM 309 332
FT DOMAIN 333 366
FT CYTOPLASMIC TAIL.
FT DISULFID 125 192
FT BY SIMILARITY.
FT DISULFID 227 283
FT BY SIMILARITY.
FT CARBOHYD 110 110
FT BY SIMILARITY.
SQ SEQUENCE 366 AA; 40842 MW; 98538EE9 CRC32;
Found using 'seq1' (seq1.key)
...
89 qkykrqatdvrslnrlrgyynqseagst
99 108
...
1 match found in sequence:
1C02.HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0102 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1C02.HUMAN STANDARD; PRT; 366 AA.
AC P30500;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0102 ALPHA CHAIN
DE PRECURSOR (CW1.2).
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERT J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., FARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84171; G187863; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-1 CW*0102.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308
FT EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 333
FT CONNECTING PEPTIDE.
FT DOMAIN 334 366
FT CYTOPLASMIC TAIL.
FT DISULFID 125 188
FT BY SIMILARITY.
FT DISULFID 227 283
FT BY SIMILARITY.
FT CARBOHYD 110 110
FT BY SIMILARITY.
SQ SEQUENCE 366 AA; 40950 MW; A19B2984 CRC32;
Found using 'seq1' (seq1.key)
...
89 qkykrqatdvrslnrlrgyynqseagst
99 108
...
1 match found in sequence:
1C05.HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0301 ALPHA CHAIN
(from "Swiss-Prot 34")

```

```

ID 1C05_HUMAN STANDARD; PRT; 366 AA.
AC P04222;
DT 20-MAR-1987 (REL. 04, CREATED)
DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0301 ALPHA CHAIN
DE PRECURSOR (CW3.1).
GN HLAC.

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84207947.
RA SODOYER R., DAMOTTE M., DELOVITCH T.L., TRUCY J., JORDAN B.R.,
RA STRACHAN T.;
RL EMBO J. 3:879-885(1984).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X00495; G642239; -
DR PIR; A02190; HLHW3.
DR HSP; P03989; ILSA.
DR MIM; 142840; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-3 CW*0301.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SO SEQUENCE 366 AA; 40744 MW; 53795742 CRC32;
Found using 'seq1' (seq1.key)

...

89 qkykpaqtdrsvlnlrqynqseqagshi
99 108
...

1 match found in sequence:
1C06_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0302 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1C06_HUMAN STANDARD; PRT; 366 AA.
AC P30503;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0302 ALPHA CHAIN
DE PRECURSOR (CW3.2).
GN HLAC.

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., PARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84174; G187869; -
DR HSP; P03989; ILSA.
DR MIM; 142840; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-3 CW*0302.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SO SEQUENCE 366 AA; 40744 MW; 53795742 CRC32;
Found using 'seq1' (seq1.key)

...

89 qkykpaqtdrsvlnlrqynqseqagshi
99 108
...

1 match found in sequence:
1C12_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1C12_HUMAN STANDARD; PRT; 366 AA.
AC P30505;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
DE PRECURSOR (CW8.1).
GN HLAC.

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., PARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84174; G187869; -
DR HSP; P03989; ILSA.
DR MIM; 142840; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-8 CW*0801.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SO SEQUENCE 366 AA; 40772 MW; A59EF965 CRC32;
Found using 'seq1' (seq1.key)

...

```

```

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84172; G187865; -
DR HSP; P03989; ILSA.
DR MIM; 142840; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-3 CW*0302.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SO SEQUENCE 366 AA; 40784 MW; C1B041C6 CRC32;
Found using 'seq1' (seq1.key)

...

89 qkykpaqtdrsvlnlrqynqseqagshi
99 108
...

1 match found in sequence:
1C12_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1C12_HUMAN STANDARD; PRT; 366 AA.
AC P30505;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
DE PRECURSOR (CW8.1).
GN HLAC.

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., PARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84174; G187869; -
DR HSP; P03989; ILSA.
DR MIM; 142840; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-8 CW*0801.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SO SEQUENCE 366 AA; 40772 MW; A59EF965 CRC32;
Found using 'seq1' (seq1.key)

...

```

Found using 'seq1' (seq1.key)

```
...
89 qkykrqatdrvslrnlrgyngseagsh
99 |-----|
108
```

1 match found in sequence:
1C13_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0802 ALPHA CHAIN
(from "Swiss-Prot 34")

```
ID 1C13_HUMAN STANDARD; PRT; 366 AA.
AC P30506;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0802 ALPHA CHAIN
DE PRECURSOR (CW8.2).
GN HLAC.
```

```
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
```

```
RN [1]
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., PARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
```

```
CC EMBL; M84173; G187867; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN CW-8 CW*0802.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 333 CONNECTING PEPTIDE.
FT DOMAIN 334 366 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 366 AA; 40871 MW; 450BD038 CRC32;
```

Found using 'seq1' (seq1.key)

```
...
89 qkykrqatdrvslrnlrgyngseagsh
99 |-----|
108
```

1 match found in sequence:
1C14_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0803 ALPHA CHAIN
(from "Swiss-Prot 34")

```
ID 1C14_HUMAN STANDARD; PRT; 366 AA.
AC P30507;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0803 ALPHA CHAIN
```

DE PRECURSOR.

```
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
```

```
RN [1]
RX MEDLINE; 92269955.
```

```
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
```

```
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
```

```
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
```

```
CC EMBL; 215144; G28357; -.
DR HSSP; P03989; 1HSA.
```

```
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
```

```
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN CW-8 CW*0803.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 333 CONNECTING PEPTIDE.
FT DOMAIN 334 366 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 366 AA; 40872 MW; F54756A6 CRC32;
```

Found using 'seq1' (seq1.key)

```
...
89 qkykrqatdrvslrnlrgyngseagsh
99 |-----|
108
```

1 match found in sequence:

1C15_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1201 ALPHA CHAIN PRECU
(from "Swiss-Prot 34")

```
ID 1C15_HUMAN STANDARD; PRT; 366 AA.
```

```
AC P30508;
```

```
DT 01-APR-1993 (REL. 25, CREATED)
```

```
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
```

```
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
```

```
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1201 ALPHA CHAIN PRECURSOR  
(HLA-CX52).
```

```
GN HLAC.
```

```
OS HOMO SAPIENS (HUMAN).
```

```
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
```

```
OC EUTHERIA; PRIMATES.
```

```
RN [1]
```

```
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE; 88330144.
```

```
RA TAKATA H., INOKO H., ANDO A., HARANAKA M., WATANABE B., TSUJI K.,
```

```
RA IRI H.;
```

```
RL IMUNOGENETICS 28:265-270(1988).
```

```
RN [2]
```

```
RP SEQUENCE FROM N.A.
```

```
RA TAKATA H., SONODA A., BECK S., HEYES J.M., BODMER J.G., INOKO H.;
```

```
RL SUBMITTED (JUN-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
```

```
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
```

```
CC THE IMMUNE SYSTEM.
```

```
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
```

```
CC EMBL; M21963; G188541; -.
```

```

DR HSPP; P03989; ILSA.
DR MIM; 142840;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 366 AA; 40855 MW; 0E9BB9A5 CRC32;
Found using 'seq1' (seq1.key)
...

89 qkykrqaqdrsvlnrlrgyngseagsh
108
...

1 match found in sequence:
1C17_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECU
(from "Swiss-Prot 34")
ID 1C17_HUMAN STANDARD; PRT; 366 AA.
AC P30510;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECURSOR
GN HLA-CB-1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86033791.
RA DAVIDSON W.F., KRESS M., KHOURY G., JAY G.;
RL J. BIOL. CHEM. 260:13414-13423(1985).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M11886; G386777;
DR PIR; A24512; HLHUC4.
DR HSSP; P03989; ILSA.
DR MIM; 142840;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 25 90
FT DOMAIN 91 182
FT DOMAIN 183 274
FT DOMAIN 275 284
FT TRANSMEM 285 309
FT DOMAIN 310 342
FT CARBOHYD 86 86
FT DISULFID 164 203
SQ SEQUENCE 342 AA; 38082 MW; CD5F7D52 CRC32;
Found using 'seq1' (seq1.key)
...

89 qkykrqaqdrsvlnrlrgyngseagsh
108
...

1 match found in sequence:
1C17_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECU
(from "Swiss-Prot 34")
ID 1C17_HUMAN STANDARD; PRT; 366 AA.
AC P30510;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECURSOR
GN HLA-CB-1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89309827.
RA TAKIGUCHI M., NISHIMURA I., HAYASHI H., KARAKI S., KARIYONE A.,
RA KANO K.;
RL J. IMMUNOL. 143:1372-1378(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M28171; G386905;
DR HSSP; P03989; ILSA.
DR MIM; 142840;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 366 AA; 40855 MW; 05F828B2 CRC32;
Found using 'seq1' (seq1.key)
...

```

```

89 qkykrqaqdrsvlnrlrgyngseagsh
108
...

1 match found in sequence:
1CX_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN.
(from "Swiss-Prot 34")
ID 1CX_HUMAN STANDARD; PRT; 342 AA.
AC P10321;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN.
GN HLA-C.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86033791.
RA DAVIDSON W.F., KRESS M., KHOURY G., JAY G.;
RL J. BIOL. CHEM. 260:13414-13423(1985).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M11886; G386777;
DR PIR; A24512; HLHUC4.
DR HSSP; P03989; ILSA.
DR MIM; 142840;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 25 90
FT DOMAIN 91 182
FT DOMAIN 183 274
FT DOMAIN 275 284
FT TRANSMEM 285 309
FT DOMAIN 310 342
FT CARBOHYD 86 86
FT DISULFID 164 203
SQ SEQUENCE 342 AA; 38082 MW; CD5F7D52 CRC32;
Found using 'seq1' (seq1.key)
...

65 qkykrqaqdrsvlnrlrgyngseagsh
75
84
...

1 match found in sequence:
HALL_MOUSE; H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-B ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")
ID HALL_MOUSE STANDARD; PRT; 362 AA.
AC P01899;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-B ALPHA CHAIN PRECURSOR.
GN H2-D.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX MEDLINE; 88060499.

```

RA WATTS S., VOGEL J.M., HARRIMAN W.D., ITOH T., STAUSS H.J.,
 RA GOODENOW R.S.;
 RL J. IMMUNOL. 139:3878-3885(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD/LT;
 RA GIRGIS K.R., CAPRA D.J., STROYNOWSKI I.;
 RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [3]
 RP SEQUENCE OF 105-362 FROM N.A.
 RX MEDLINE; 83005712.
 RA REYES A.A., SCHOLD M., WALLACE R.B.;
 RL IMMUNOGENETICS 16:1-9(1982).
 RN [4]
 RP SEQUENCE OF 25-122.
 RX MEDLINE; 81142266.
 RA MALOY W.L., NATHENSON S.G., COLIGAN J.E.;
 RL J. BIOL. CHEM. 256:2863-2872(1981).
 RN [5]
 RP SEQUENCE OF 253-308 AND 332-358.
 RX MEDLINE; 83005713.
 RA MALOY W.L., COLIGAN J.E.;
 RL IMMUNOGENETICS 16:11-22(1982).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 25-296.
 RX MEDLINE; 94116065.
 RA YOUNG A.C.M., ZHANG W., SACCHETTINI J.C., NATHENSON S.G.;
 RL CELL 76:39-50(1994).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 DR EMBL; M18523; G387452; -.
 DR EMBL; L36068; G797272; -.
 DR EMBL; K00129; G199341; ALT_INIT.
 DR PIR; A02200; HLMSDB.
 DR PDB; 1HOC; 30-APR-94.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
 FT SIGNAL 1 24
 FT CHAIN 25 362
 FT
 FT DOMAIN 25 114
 FT DOMAIN 115 206
 FT DOMAIN 207 298
 FT DOMAIN 299 309
 FT DOMAIN 310 331
 FT DOMAIN 332 362
 FT DISULFID 125 188
 FT DISULFID 227 283
 FT CARBOHYD 110 110
 FT CARBOHYD 200 200
 FT CARBOHYD 280 280
 FT STRAND 27 36
 FT STRAND 47 51
 FT STRAND 56 61
 FT TURN 62 63
 FT TURN 70 71
 FT TURN 75 76
 FT TURN 77 79
 FT TURN 81 81
 FT TURN 82 109
 FT TURN 110 110
 FT STRAND 118 127
 FT TURN 129 130
 FT STRAND 133 142
 FT TURN 143 144
 FT STRAND 145 150
 FT TURN 152 153
 FT TURN 157 159
 FT TURN 163 163
 FT HELIX 164 173
 FT TURN 174 175

FT HELIX 176 185
 FT TURN 186 186
 FT HELIX 187 196
 FT TURN 197 198
 FT TURN 200 204
 FT STRAND 210 210
 FT STRAND 213 213
 FT TURN 220 221
 FT STRAND 225 232
 FT STRAND 238 243
 FT TURN 244 245
 FT STRAND 246 247
 FT TURN 250 251
 FT STRAND 253 254
 FT STRAND 258 259
 FT STRAND 265 271
 FT TURN 275 276
 FT TURN 278 279
 FT STRAND 281 286
 FT TURN 288 289
 SQ SEQUENCE 362 AA; 40836 MW; 6C5B86B5 CRC32;
 Found using 'seq1' (seq1.key)
 ...
 89 qkxgqeqwfrvsrlnllgynqsagshs
 99 108
 ID HA14_MOUSE STANDARD; PRT; 368 AA.
 AC P14427;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-P ALPHA CHAIN PRECURSOR.
 GN H2-D.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA.
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86169714.
 RA SCHEPARD B.S., TAKAHASHI H., COZAD K.M., MURRAY R., OZATO K.,
 RA APPELLA E., FRELINGER J.A.;
 RL J. IMMUNOL. 136:3489-3495(1986).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 DR EMBL; M12381; G387454; -.
 DR HSSP; P01901; IYAA.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 21
 FT CHAIN 22 368
 FT
 FT DOMAIN 22 111
 FT DOMAIN 112 203
 FT DOMAIN 204 295
 FT DOMAIN 296 300
 FT TRANSMEM 304 330
 FT DOMAIN 331 368
 FT DISULFID 122 185
 FT DISULFID 224 280
 FT CARBOHYD 107 107
 FT CARBOHYD 197 197
 FT CARBOHYD 277 277

1 match found in sequence:

HA14_MOUSE ; H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-P ALPHA CHAIN PRECURSOR
 (from "Swiss-Prot 34")

ID HA14_MOUSE STANDARD; PRT; 368 AA.

AC P14427;

DT 01-JAN-1990 (REL. 13, CREATED)

DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-P ALPHA CHAIN PRECURSOR.

GN H2-D.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA.

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 86169714.

RA SCHEPARD B.S., TAKAHASHI H., COZAD K.M., MURRAY R., OZATO K.,

RA APPELLA E., FRELINGER J.A.;

RL J. IMMUNOL. 136:3489-3495(1986).

CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMUNE SYSTEM.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN).

DR EMBL; M12381; G387454; -.

DR HSSP; P01901; IYAA.

DR PROSITE; PS00290; IG_MHC.

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

FT SIGNAL 1 21

FT CHAIN 22 368

FT

FT DOMAIN 22 111

FT DOMAIN 112 203

FT DOMAIN 204 295

FT DOMAIN 296 300

FT TRANSMEM 304 330

FT DOMAIN 331 368

FT DISULFID 122 185

FT DISULFID 224 280

FT CARBOHYD 107 107

FT CARBOHYD 197 197

FT CARBOHYD 277 277

SQ SEQUENCE 368 AA; 41342 MW; 7D4C13C1 CRC32;
Found using 'seq1' (seq1.key)

...

86 qnakdhegsfrvslrnllygnqskgsht
96 105

...

1 match found in sequence:
HLAH_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")
ID HLAH_HUMAN STANDARD; PRT; 362 AA.
AC P01893;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
DE (HLA-AR) (HLA-12.4).
GN HLAH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82151002.
RA MALISSEN M., MALISSEN B., JORDAN B.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).
CC !- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC !- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC EMBL; V00526; G386873; ALT_INIT.
DR PIR; A02189; HLH12.
DR HSP; P03989; 1HSA.
DR MIM; 142925; .
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN H.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40850 MW; 5E610F63 CRC32;
Found using 'seq1' (seq1.key)

...

89 qickagaqternlrlyalryngqsgsht
99 108

...

-- Search Statistics --
Times: CPU Total Elapsed
00:03:44.14 00:04:09.00
Number of sequences searched: 241556
Number of sequence hits: 232
Number of separate matches: 232
Number of sequence hits saved: 0

THIS PAGE BLANK (USPTO)

WATER (TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
Copyright (C) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:45:38 1997; MasPar time 1.81 Seconds
Tabular output not generated. 70.334 Million cell updates/sec

Title: >US-08-653-294-7
Description: (1-6) from US08653294.pep
Perfect Score: 49
Sequence: 1 YRLAIR 6

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 22.440; Variance 22.471; scale 0.999

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | | | | |
|--------|-------|-------|--------|----|-------------|
| No. | Score | Match | Length | ID | Description |
| | | | | | Pred. No. |

No matches found.

Search completed: Thu May 22 08:45:46 1997
Job time : 8 secs.

THIS PAGE BLANK (USPTO)

W P S R E L A (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:50:08 1997; MasPar time 2.66 Seconds
128.376 Million cell updates/sec
Tabular output not generated.

Title: >US-08-653-294-36
Description: (1-12) from US08653294.pep
Perfect Score: 98
Sequence: 1 YRLAIRRIALRY 12

Scoring table: PAM 150
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 26.905; Variance 45.950; scale 0.586

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | Score | Match | Length | ID | Description | Pred. No. |
|--------|-------|-------|-------|--------|----|-------------|-----------|
|--------|-------|-------|-------|--------|----|-------------|-----------|

No matches found.

Search completed: Thu May 22 08:50:18 1997
Job time : 10 secs.

THIS PAGE BLANK (USPTO)

MPERCH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:49:45 1997; MasPar time 1.88 Seconds
Tabular output not generated. 135.656 Million cell updates/sec

Title: >US-08-653-294-36
Description: (1-12) from US08653294.pep
Perfect Score: 98
Sequence: 1 YRLAIRRLRY 12

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 60

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 28.088; Variance 37.415; scale 0.751

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | | | | |
|--------|-------|-------|--------|----|-------------|
| No. | Score | Match | Length | ID | Description |
| | | | | | Pred. No. |

No matches found.

Search completed: Thu May 22 08:49:51 1997
Job time : 6 secs.

THIS PAGE BLANK (USPTO)

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:26:14 1997; MasPar time 2.05 Seconds
Tabular output not generated. 61.975 Million cell updates/sec

Title: >US-08-653-294-4
Description: (1-6) from US08653294.p
Perfect Score: 49
Sequence: 1 RIALRY 6

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 22.521; Variance 22.707; scale 0.992

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 49 | 100.0 | 359 | 1 | 1B01_PANTR CHLA CLASS I HISTOCOMP | 5.42e-01 |
| 2 | 49 | 100.0 | 362 | 1 | 1B49_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 3 | 49 | 100.0 | 362 | 1 | 1B01_GORGO CLASS I HISTOCOMP | 5.42e-01 |
| 4 | 49 | 100.0 | 362 | 1 | 1B47_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 5 | 49 | 100.0 | 362 | 1 | 1B52_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 6 | 49 | 100.0 | 362 | 1 | 1B03_GORGO CLASS I HISTOCOMP | 5.42e-01 |
| 7 | 49 | 100.0 | 362 | 1 | 1B02_GORGO CLASS I HISTOCOMP | 5.42e-01 |
| 8 | 49 | 100.0 | 362 | 1 | 1B15_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 9 | 49 | 100.0 | 362 | 1 | 1B54_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 10 | 49 | 100.0 | 362 | 1 | 1B62_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 11 | 49 | 100.0 | 362 | 1 | 1B61_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 12 | 49 | 100.0 | 362 | 5 | HLAH_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 13 | 49 | 100.0 | 362 | 1 | 1B53_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 14 | 49 | 100.0 | 362 | 1 | 1B60_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 15 | 49 | 100.0 | 365 | 1 | 1A04_GORGO CLASS I HISTOCOMP | 5.42e-01 |
| 16 | 49 | 100.0 | 365 | 1 | 1A23_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 17 | 49 | 100.0 | 365 | 1 | 1A32_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 18 | 49 | 100.0 | 365 | 1 | 1A24_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 19 | 49 | 100.0 | 365 | 1 | 1A25_HUMAN HLA CLASS I HISTOCOMP | 5.42e-01 |
| 20 | 46 | 93.9 | 409 | 1 | AA2A_CAVPO ADENOSINE A2A RECEPTO | 2.89e+00 |
| 21 | 46 | 93.9 | 410 | 1 | AA2A_RAT ADENOSINE A2A RECEPTO | 2.89e+00 |
| 22 | 46 | 93.9 | 412 | 1 | AA2A_HUMAN ADENOSINE A2A RECEPTO | 2.89e+00 |

| | | | | | | |
|----|----|------|------|----|-----------------------------------|----------|
| 23 | 46 | 93.9 | 412 | 1 | AA2A_CANFA ADENOSINE A2A RECEPTO | 2.89e+00 |
| 24 | 46 | 93.9 | 1420 | 1 | APOA_MACMU APOLIPOPROTEIN(A) (EC | 2.89e+00 |
| 25 | 45 | 91.8 | 383 | 6 | MEYA_PSEAE MULTIDRUG RESISTANCE | 4.96e+00 |
| 26 | 45 | 91.8 | 462 | 2 | COXA_YEAST CYTOCHROME C OXIDASE | 4.96e+00 |
| 27 | 45 | 91.8 | 880 | 8 | RNA1_SULAC DNA-DIRECTED RNA POLY | 4.96e+00 |
| 28 | 45 | 91.8 | 959 | 6 | MSH1_YEAST MUTS PROTEIN HOMOLOG | 4.96e+00 |
| 29 | 45 | 91.8 | 1726 | 8 | RPB1_YEAST DNA-DIRECTED RNA POLY | 4.96e+00 |
| 30 | 45 | 91.8 | 1752 | 8 | RPB1_SCHPO DNA-DIRECTED RNA POLY | 4.96e+00 |
| 31 | 45 | 91.8 | 2225 | 8 | PYR1_HUMAN CAD PROTEIN (CONTAINS | 4.96e+00 |
| 32 | 45 | 91.8 | 2225 | 8 | PYR1_MESAU CAD PROTEIN (CONTAINS | 4.96e+00 |
| 33 | 44 | 89.8 | 85 | 10 | V192_BPT7 GENE 19.2 PROTEIN. | 8.43e+00 |
| 34 | 44 | 89.8 | 332 | 1 | AA2B_RAT ADENOSINE A2B RECEPTO | 8.43e+00 |
| 35 | 44 | 89.8 | 638 | 1 | 60IM_COXBU 60 KD INNER-MEMBRANE | 8.43e+00 |
| 36 | 44 | 89.8 | 953 | 2 | COBP_RAT COATOMER BETA SUBUNIT | 8.43e+00 |
| 37 | 43 | 87.8 | 646 | 6 | LEPA_MYCLE GTP-BINDING PROTEIN L | 1.42e+01 |
| 38 | 43 | 87.8 | 767 | 5 | HREB_ECOLI ATP-DEPENDENT HELICASE | 1.42e+01 |
| 39 | 43 | 87.8 | 817 | 8 | RRPO_CRV PROBABLE RNA-DIRECTED | 1.42e+01 |
| 40 | 43 | 87.8 | 817 | 8 | RRPO_CNV PROBABLE RNA-DIRECTED | 1.42e+01 |
| 41 | 43 | 87.8 | 817 | 8 | RRPO_TBSVC PROBABLE RNA-DIRECTED | 1.42e+01 |
| 42 | 43 | 87.8 | 968 | 4 | HEPA_ECOLI PROBABLE ATP-DEPENDEN | 1.42e+01 |
| 43 | 43 | 87.8 | 1859 | 8 | RPB1_CAEEL DNA-DIRECTED RNA POLY | 1.42e+01 |
| 44 | 42 | 85.7 | 436 | 10 | VU10_HSV6U U10 PROTEIN. | 2.36e+01 |
| 45 | 42 | 85.7 | 1165 | 3 | CYA6_CANFA ADENYLATE CYCLASE, TY | 2.36e+01 |

ALIGNMENTS

RESULT 1
ID 1B01_PANTR STANDARD; PRT; 359 AA.

AC P13750;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
DE (FRAGMENT).
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89030641.
RA MAYER W.E.; JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
RA KLEIN J.;
RL EMBO J. 7:2765-2774(1988).
RN [2]
RP REVISIONS.
RA MAYER W.;
RL SUBMITTED (FEB-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; X13115; G755776; -.
DR FIR; S03537; S03537.
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT NON_TER 1
FT SIGNAL <1 20
FT CHAIN 21 359
FT DOMAIN 110
FT DOMAIN 111
FT DOMAIN 202
FT DOMAIN 203
FT DOMAIN 295
FT DOMAIN 306
FT DOMAIN 329
FT DOMAIN 330
FT DOMAIN 359
FT DISULFID 121
FT DISULFID 184
FT DISULFID 223
FT CARBOHYD 106
SQ SEQUENCE 359 AA; 40173 MW; 53955FFC9 CRC32;
Query Match 100.0%; Score 49; DB 1; Length 359;

Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rialry 104
| | | | |
QY 1 RIALRY 6

RESULT 2
ID 1B49 HUMAN STANDARD; PRT: 362 AA.
AC P18464;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*51(B-5) B*5101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89233295.
RA POHLA H., KOON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
RL IMMUNOGENETICS 29:297-307(1989).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M22792; G553533; ALT_SEQ.
DR EMBL; M22786; G553533; JOINED.
DR EMBL; M22787; G553533; JOINED.
DR EMBL; M22788; G553533; JOINED.
DR EMBL; M22789; G553533; JOINED.
DR EMBL; M22790; G553533; JOINED.
DR EMBL; M22791; G553533; JOINED.
DR EMBL; L41087; G735902; -.
DR EMBL; L41086; G735902; JOINED.
DR PIR; A30345; A30345.
DR PIR; A30548; A30548.
DR HSP; P03989; ILSA.
DR MIM; I42830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B*51(B-5) B*5101.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT FT 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
| | | | |
QY 1 RIALRY 6

RESULT 3
ID 1B01 GORGO STANDARD; PRT: 362 AA.
AC P30379;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; X60255; G22866; -.
DR PIR; JH0539; JH0539.
DR HSP; P03989; ILSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-B0101 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
| | | | |
QY 1 RIALRY 6

RESULT 4
ID 1B47 HUMAN STANDARD; PRT: 362 AA.
AC P30487;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*49(B-21) B*4901 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
RN [2]
RP REVISIONS TO 78.
RX MEDLINE; 93056529.

RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
 RA WILLIAMS R.C., PARHAM P.;
 RL J. IMMUNOL. 149:3563-3568(1992).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 DR EMBL; M24037; G407191; -.
 DR HSSP; P03989; ILSA.
 DR MIM; 142830; -.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN B-49(B-21) B*4901.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 299 309 CONNECTING PEPTIDE.
 FT TRANSMEM 310 333
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;
 Query Match 100.0%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 103 rialry 108
 QY 1 RIALRY 6
 RESULT 5
 ID 1B52_HUMAN STANDARD; PRT; 362 AA.
 AC P30489;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
 DE PRECURSOR.
 GN HLAB.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92269955.
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
 RL NATURE 357:326-329(1992).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 DR EMBL; Z15143; G28235; -.
 DR HSSP; P03989; ILSA.
 DR MIM; 142830; -.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT ALPHA CHAIN B-51(B-5) B*5104.
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 299 308 CONNECTING PEPTIDE.
 FT DOMAIN 309 332
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT CARBOHYD 110 110 BY SIMILARITY.
 FT DISULFID 125 188 BY SIMILARITY.

FT DISULFID 227 283 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;
 Query Match 100.0%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 103 rialry 108
 QY 1 RIALRY 6
 RESULT 6
 ID 1B03_GORGO STANDARD; PRT; 362 AA.
 AC P30381;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
 OS GORILLA GORILLA (LOWLAND GORILLA).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92078860.
 RA LAWOR D.A., WARREN E., TAYLOR P., PARHAM P.;
 RL J. EXP. MED. 174:1491-1509(1991).
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 DR EMBL; X60254; G22870; -.
 DR PIR; JH0541; JH0541.
 DR HSSP; P03989; ILSA.
 DR PROSITE; PS00290; IG_MHC.
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 362 BY SIMILARITY.
 FT DOMAIN 25 114 GOGO-B0103 ALPHA CHAIN.
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 309 332 CONNECTING PEPTIDE.
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.
 FT DISULFID 125 188 BY SIMILARITY.
 FT DISULFID 227 283 BY SIMILARITY.
 FT CARBOHYD 110 110 BY SIMILARITY.
 SQ SEQUENCE 362 AA; 40248 MW; FEA6A941 CRC32;
 Query Match 100.0%; Score 49; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 103 rialry 108
 QY 1 RIALRY 6
 RESULT 7
 ID 1B02_GORGO STANDARD; PRT; 362 AA.
 AC P30380;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
 OS GORILLA GORILLA (LOWLAND GORILLA).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92078860.
 RA LAWOR D.A., WARREN E., TAYLOR P., PARHAM P.;

RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X60693; G22868; -.
DR PIR; JH0540; JH0540.
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT TRANSMEM 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40204 MW; 3CF119AD CRC32;
Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 103 rialry 108
QY 1 RIALRY 6
RESULT 8
ID 1B15_HUMAN STANDARD; PRT; 362 AA.
AC P10317;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
DE PRECURSOR (B-27K) (B27.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86220133.
RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
RL EMBO J. 5:547-552(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA FARHAM P., ARNETT K.L., ADAMS E.J.;
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE OF 86-107 AND 171-181.
RX MEDLINE; 86042671.
RA VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
RA LOPEZ DE CASTRO J.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 82:7394-7398(1985).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X03684; G871296; -.
DR EMBL; X03667; G871296; JOINED.
DR EMBL; L38504; G896271; -.
DR PIR; B25092; HLHUBK.
DR HSSP; P03989; 1HSA.
DR MIM; 142830;
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24

FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT TRANSMEM 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40397 MW; 9798F0BB CRC32;
Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 103 rialry 108
QY 1 RIALRY 6
RESULT 9
ID 1B54_HUMAN STANDARD; PRT; 362 AA.
AC P30491;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91033941.
RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,
RA TAKIGUCHI M.;
RL IMMUNOGENETICS 32:195-199(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M58336; G187757; -.
DR PIR; A45834; A45834.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT TRANSMEM 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;
Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 103 rialry 108
QY 1 RIALRY 6

```

RESULT 10
ID 1B62_HUMAN STANDARD; PRT; 362 AA.
AC P10319;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN). CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 86008247.
RA WAYS J.P., COPPIN H.L., PARHAM P.;
RL J. BIOL. CHEM. 260:11924-11933(1985).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M11799; G386885; -.
DR PIR; A23895; HLH08.
DR MIN; 142830; -.
DR HSSP; P03989; IHSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B*57(B-17) B*5702.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40337 MW; 35E57534 CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
Qy 1 RIALRY 6

RESULT 12
ID HLAH_HUMAN STANDARD; PRT; 362 AA.
AC P01893;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
DE (HLA-AR) (HLA-12.4).
GN HLAH.
OS HOMO SAPIENS (HUMAN). CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 82151002.
RA MALISEN M., MALISEN B., JORDAN B.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; V00526; G386873; ALT_INIT.
DR PIR; A02189; HLH012.
DR HSSP; P03989; IHSA.
DR MIN; 142925; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN H.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40850 MW; 5E610F63 CRC32;

Query Match 100.0%; Score 49; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
Qy 1 RIALRY 6

RESULT 11
ID 1B61_HUMAN STANDARD; PRT; 362 AA.
AC P30497;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*57(B-17) B*5702 ALPHA CHAIN
DE PRECURSOR (BW57.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN). CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.M., ZEMOUR J., ENNIS P.D., WARD F.E., PETEL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).

```

```

DR EMBL; X61707; G32187; -.
DR PIR; S16774; S16774.
DR HSSP; P03989; IHSA.
DR MIN; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B*57(B-17) B*5702.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 628C2156 CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
Qy 1 RIALRY 6

RESULT 12
ID HLAH_HUMAN STANDARD; PRT; 362 AA.
AC P01893;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
DE (HLA-AR) (HLA-12.4).
GN HLAH.
OS HOMO SAPIENS (HUMAN). CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 82151002.
RA MALISEN M., MALISEN B., JORDAN B.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; V00526; G386873; ALT_INIT.
DR PIR; A02189; HLH012.
DR HSSP; P03989; IHSA.
DR MIN; 142925; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN H.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40850 MW; 5E610F63 CRC32;

Query Match 100.0%; Score 49; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
Qy 1 RIALRY 6

```

```

Db 103 r1alry 108
QY 1 RIALRY 6

RESULT 13
ID 1B53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M22799; G553538; ALT_SEQ.
DR EMBL; M22793; G553538; JOINED.
DR EMBL; M22794; G553538; JOINED.
DR EMBL; M22795; G553538; JOINED.
DR EMBL; M22796; G553538; JOINED.
DR EMBL; M22797; G553538; JOINED.
DR EMBL; M22798; G553538; JOINED.
DR PIR; B30345; B30345.
DR PIR; B30548; B30548.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 1 24
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40521 MW; 3B436FE8 CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 r1alry 108
QY 1 RIALRY 6

RESULT 14
ID 1B60_HUMAN STANDARD; PRT; 362 AA.
AC P18465;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*57(B-17) B*5701 ALPHA
DE CHAIN PRECURSOR (BW57.1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).

```

```

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RX SEQUENCE FROM N.A.
RA MEDLINE; 91067476.
RA ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
RL NUCLEIC ACIDS RES. 18:6702-6702(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M32318; G307222; -.
DR EMBL; X55711; G32181; -.
DR PIR; S12622; S12622.
DR PIR; D35997; D35997.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40224 MW; D91DF8DD CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 r1alry 108
QY 1 RIALRY 6

RESULT 15
ID 1A04_GORGO STANDARD; PRT; 365 AA.
AC P30378;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-A0501 ALPHA CHAIN PRECURSOR.
DE GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X60256; G22860; -.
DR PIR; JH0537; JH0537.
DR HSP; P01892; IHHG.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 365

```

FT DOMAIN 25 114 GOGO-A0501 ALPHA CHAIN.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 288 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 365 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 365 AA; 40895 MW; 520225DF CRC32;

Query Match 100.0%; Score 49; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
QY 1 RIALRY 6

Search completed: Thu May 22 08:26:26 1997
Job time : 12 secs.

THIS PAGE BLANK (USPTO)